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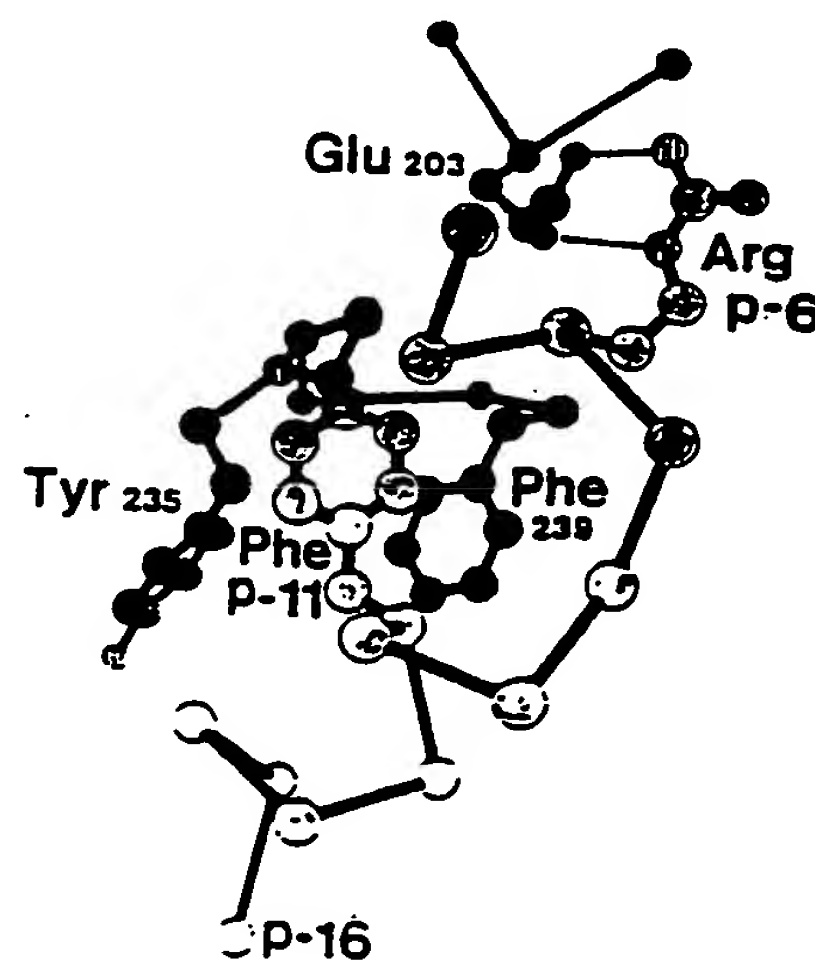
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(54) Title: METHODS OF DESIGNING SPECIFIC AFFECTORS USING THREE-DIMENSIONAL CONFORMATION OF ENZYME/AFFECTOR COMPLEX

## (57) Abstract

The present invention includes methods for rational drug design. One exemplary method disclosed herein teaches the preparation of a highly specific affector of a first enzyme when the first enzyme is a member of a class of enzymes having a conserved catalytic core with a plurality of invariant residues. This method comprises identifying a second enzyme that is a member of that class of enzymes and has a known affector. The affector can be an inhibitor or activator of the second enzyme. In the practise of the method, a first complex is formed between the second enzyme and the known affector and data is obtained regarding the three-dimensional coordinates of the invariant residues in the complex. These coordinates are used to form a template. A model is then generated in which the first enzyme is in a conformation with the invariant residues in substantially the same conformation as in the template. Changes in the variable residues of the catalytic core of the first enzyme are compared to the variable residues in the catalytic core of the second enzyme. The second enzyme is modified to include these non-conserved changes and an affector is designed using computer modelling that will induce a conformation on the catalytic core of the first enzyme in which the invariant residues are in substantially the same coordinates as the coordinates of the template when the first enzyme is formed as a second complex with the newly designed affector. The designed affector can be further refined to provide improved affector activity.



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## METHODS OF DESIGNING SPECIFIC AFFECTORS USING THREE DIMENSIONAL CONFORMATION OF ENZYME/AFFECTOR COMPLEX

### Field of the Invention

5 The present invention relates to rational design of specific affectors for a given enzyme using data obtained regarding the three dimensional conformation of an enzyme/affecter complex. More particularly, it relates to such methods wherein the conformation of the conserved catalytic core of a given enzyme class is elucidated and highly specific affector molecules for a particular member of that class are designed.

### Background of the Invention

10 Drug design based on an analysis of the structural features of a molecule is still in its infancy. At present, an analysis of X-ray crystallographic data at best permits the design of broadly acting affector molecules. While these affector molecules can be further refined to impart some selectivity, affector design does not produce molecules having the fine tuned specificity of, for example, an antibody for its antigen. This level of selectivity control is not  
15 always necessary; however, therapeutic regimes directed to the control of enzymes involved in certain cancers, genetic disorders, and infectious agents will require this type of selectivity.

Enzymes can be classified into broad families or classes having similar activities, with each enzyme having a specific function. For example, many proteins phosphorylate their  
20 substrate. These enzymes are broadly labelled as kinases. A myriad of kinases exist for a myriad of functions. Within this broad group, kinases can be subgrouped based on similarities in substrate, requirements for additional cofactors or similar amino acid residues that are targets for phosphorylation.

Within any given cell, there may be many active members of a given enzyme family.  
25 If one member of the family shows aberrant activity, then it may be therapeutically advantageous to alter the activity of this single enzyme to the exclusion of other similar or related enzymes. Such is the case for the protein kinase family where aberrant phosphorylation events can be associated with abnormal cell growth and regulation. This is observed in proto-oncogene related cancers. For example, the pp60<sup>c-src</sup> protein, needs  
30 to be controlled to the exclusion of other protein kinases in order to maintain normal cell metabolism.

Protein phosphorylation as a mechanism for regulating protein activity was first recognized in 1955 with glycogen phosphorylase. Protein phosphorylation and dephosphorylation is widespread and impacts nearly all aspects of growth and homeostasis

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in the eukaryotic cell. Protein kinases catalyze the transfer of the  $\gamma$ -phosphate of MgATP to a protein substrate. The protein kinases, constitute a large and very diverse family of enzymes. Although these enzymes differ in size, substrate specificity, mechanism of activation, subunit composition, and subcellular localization, all, nevertheless, share a homologous catalytic core that has been conserved throughout evolution.

It is not yet possible to regulate a given enzyme at will. While there are hundreds of different protein kinases, only a few of these can be readily purified. Moreover, even among those enzymes that can be purified, many cannot be used for X-ray crystallographic studies. The sequences of many enzymes have been cloned and expressed; however, not all of these are chemically active. Therefore, even if a molecule that cannot be readily purified is cloned and expressed, it may not be functional and thus, would not provide an adequate model for structural studies. Further, even if a recombinant protein is functional, it may not be readily crystallizable. These and other roadblocks have heretofore prevented the design or identification of effector molecules directed to a particular enzyme. Thus, heretofore it has not been possible to provide a method for the design of effector molecules for a given member of an enzyme family.

#### Brief Description of the Figures

Figure 1 illustrates the general topological arrangement of the catalytic subunits from a number of different protein kinases.

Figure 2 diagrams the placement of the catalytic region within various members of the protein kinase family.

Figure 3 is a stereo view of the electron density for the structure determination. Figure 3A provides the density calculated to 2.7 Å. Figure 3B provides the density calculated with 10.0 to 2.7 Å refined model phases.

Figure 4 is a stereo view of the C- $\alpha$  backbone and includes twenty residues of PKI(5-24).

Figure 5 provides data on the location and orientation of MgATP. Figure 5A illustrates the general localization of MgATP. Figure 5B is a close-up of difference density enclosing an oriented model of AMP.

Figure 6 is an overall two dimensional topology diagram for the C-subunit. of cAPK. Figure 7 provides stereo views of selected conserved areas.

Figure 8 illustrates the conserved catalytic core of c-AMP dependent protein kinase. Figure 8A is a space-filling model of the catalytic core. Figure 8B is a diagram of the



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conserved catalytic core using the RIBBON program of the PAP package. Figure 8C is a space-filling model identical to A, but includes PKI(5-24).

Figure 9 diagrams the conformation of bound PKI (5-24).

5 Figure 10 illustrates the high affinity binding site interactions between the catalytic subunit and the inhibitor peptide. In Figure 10A the P-11 Phe ring (numbered 356) is shown in relation to three nearby hydrophobic residues of the C-subunit. Figure 10B illustrates the interactions of the P-11 Phe and P-6 Arg sidechains with the C-subunit.

Figure 11 summarizes the interactions that contribute to recognition of the common consensus region of the inhibitor peptide.

10 Figure 12 illustrates the consensus recognition site binding interactions. Figure 12A is an illustration of the electron density corresponding to the anionic P-3 site. Figure 12B illustrates the electron density of the P-2 Arg side chain. Figure 12C illustrates the electron density of the P+1 Ile sidechain.

15 Figure 13 illustrates the catalytic site area. Figure 13A provides the site of catalysis together with the probable catalytic base sidechain of Asp 166 near the  $\beta$ -C of the P Ala. Figure 13B diagrams the consensus recognition site residues Arg-Arg-Asn-Ala-Ile. Figure 13C shows the phosphate of Thr 197 buried among sidechains of cationic and H-bonding residues.

20 Figure 14 is a schematic illustrating the relationship of invariant amino acids at the active site.

Figure 15 is a schematic of the conserved and variable regions of the catalytic subunit.

Figure 16 illustrates the amino acids present in PKI(5-24) that provide important interactions with cAPK.

25 Figure 17 provides a list of the coordinates that define the three-dimensional template.

Figure 18 provides photographs of the crystal forms.

#### Summary of the Invention

30 In accordance with one aspect of the present invention, there is provided a method of designing a highly specific effector which exerts an effect on the activity of a first enzyme. In this method, the first enzyme is a member of a class of enzymes having a conserved catalytic core. The method comprises the following steps: identifying a second enzyme that is a member of the class in which a first effector can affect the activity of the second enzyme, forming a first complex of the first effector and the second enzyme, obtaining data

regarding the conformation of the second enzyme at sites greater than 5 Å from the site of catalysis of the second enzyme in the first complex, and designing an effector which induces a conformation on the first enzyme at sites greater than 5 Å from the site of catalysis thereof which is homologous to the conformation of the second enzyme at homologous sites in the first complex, when the effector is formed as a second complex with the first enzyme. Preferably, this method additionally comprises crystallizing the first complex and obtaining X-ray crystallography data therefrom. In a preferred form of this method, all of the members of the class have related functions, and the catalytic cores of all of the members of the class have conserved amino acid residues. In this form of the method, preferably the designing step comprises designing an effector having homologous topography and charge fields that complement the catalytic core of the first enzyme and capable of inducing a conformation wherein the conserved amino acid residues of the first enzyme are in homologous locations to the second enzyme in the first complex. The effectors can be inhibitors, activators or other effectors of enzyme activity. The first effector can be all or a portion of the first enzyme, and the first complex can be a holoenzyme. The class of enzymes can comprise protein kinases or any other suitable class. The second enzyme can be a viral oncogene product or a cellular homologue thereof, such as p60 v-Src from RSV or its cellular homologue, pp60 c-src. The second enzyme can also be cAMP-dependent protein kinase. The second enzyme can be a native mammalian protein kinase or a recombinant protein kinase. In a preferred form of the method, the designing step comprises identifying a potential effector likely to induce a conformation on the catalytic core of the first enzyme which is homologous to the conformation of the catalytic core of the second enzyme in the first complex, when the effector is formed as a second complex with the first enzyme, and determining whether the potential effector induces the conformation through the use of a technique selected from the group consisting of computer modelling, small angle neutron scattering, and circular dichroism. In this preferred method, the potential effector comprises a peptide, and the potential effector comprises a molecule selected from the group consisting of nucleotides, polynucleotides, alcohols, polymers, lipids carbohydrates, sugars, native or synthetic molecules, protein and organic compounds and combinations thereof. In accordance with this aspect of the invention, the method can include producing the effector. Thus, the present invention also includes the effector produced from the method.

In another aspect of the present invention, there is provided another method of designing a highly specific effector which exerts an effect on the activity of a first enzyme.

In this method, the first enzyme is also a member of a class of enzymes having conserved residues at an effector binding site. This method comprises the following steps: identifying a second enzyme that is a member of the class in which a first effector can affect the activity of the second enzyme, the first effector having a dissociation constant with the second enzyme of less than 1  $\mu$ M, forming a first complex of the first effector and the second enzyme, obtaining data regarding the conformation of the effector binding site of the second enzyme in the first complex, and designing an effector which induces a conformation on the effector binding site of the first enzyme which is homologous to the conformation of the effector binding site of the second enzyme in the first complex, when the effector is formed as a second complex with the first enzyme. In one form of this method, the class of enzymes has a nucleotide binding site and each of the effectors is capable of binding to the nucleotide binding site.

In still another aspect of the present invention, there is provided another method of designing a highly specific effector which exerts an effect on the activity of a first enzyme. In this method, the first enzyme is also a member of a class of enzymes having a conserved catalytic core. This method comprises the following steps: identifying a second enzyme that is a member of the class in which a first effector can affect the activity of the second enzyme, forming a first complex of the first effector and the second enzyme, the first complex having at least three points of contact between the first effector and second enzyme, obtaining data regarding the conformation of the catalytic core of the second enzyme in the first complex, and designing an effector which induces a conformation on the catalytic core of the first enzyme which is homologous to the conformation of the catalytic core of the second enzyme in the first complex, when the effector is formed as a second complex with the first enzyme.

Still another aspect of the present invention provides a crystallized protein kinase/effector complex having stable decay characteristics over 15 minutes and a crystallized protein kinase/effector complex having a Bragg spacing diffraction limit of less than 4 $\text{\AA}$ . Preferably, the crystallized protein kinase of this aspect of the invention exhibits both of these characteristics. The present invention also provides a crystallized complex of a cAMP-dependent protein kinase and an inhibitor thereof. This crystallized complex can be used in an X-ray crystallography procedure to produce data regarding the three dimensional structure of the cAMP-dependent protein kinase in the complex, and this data can be used for designing an inhibitor of a second protein kinase which will induce a similar three dimensional structure on the active site of the second protein kinase as the three

dimensional structure of the cAMP-dependent protein kinase in the complex. Thus, the present invention also includes an inhibitor designed by this method.

Another preferred method of the present invention involves preparing a highly specific effector of a first enzyme, with the first enzyme being a member of a class of enzymes having a conserved catalytic core with a plurality of invariant residues. This method comprises the following steps: identifying a second enzyme that is a member of the class and having a known effector thereof, forming a first complex of the second enzyme and the known effector, obtaining data regarding the three dimensional coordinates of the invariant residues in the first complex, the coordinates forming a template, generating a model wherein the first enzyme is in a conformation in which the invariant residues are in substantially the same conformation as in the template, identifying a change in the variable residues in the catalytic core of the first enzyme in the conformation of the template when compared to the variable residues in the catalytic core of the second enzyme in the conformation of the template, preparing a modified form of the second enzyme, wherein the modified second enzyme includes a non-conserved change identified through this method, and designing an effector which computer modelling indicates will induce a conformation on the catalytic core of the first enzyme in which the invariant residues are in substantially the same coordinates as the coordinates of the template, when the first enzyme is formed as a second complex with the effector designed in this step. Preferably the identified change is a non-conserved change in the variable residues. In a preferred form of this method, the method also includes forming a third complex of the modified second enzyme and an effector capable of binding thereto, obtaining data regarding the three dimensional coordinates of the invariant residues in the third complex, and using the data obtained in the previous step to design an effector which computer modelling indicates will induce a conformation on the catalytic core of the first enzyme in which the invariant residues are closer to the coordinates of the template than the conformation induced by the effector designed previously, when the first enzyme is formed as a fourth complex with the effector designed in this step. The effector used for computer modelling can be the known effector. Preferably, the method also includes modifying the computer modelling in light of the data obtained through the method prior to designing the effector. Amino acid sequence data relating to the catalytic cores of the first and second enzymes is preferably obtained. Site directed mutagenesis of a recombinantly produced second enzyme can be used in accordance with the method. In one preferred aspect of this method, the coordinates of the template are substantially as shown in Figure 17 and the template can include

coordinates separated by the distances substantially as shown in Table 4. The effectors can be inhibitors or other effectors. The method can also include preparing the designed effector. Thus, the present invention also includes the effectors prepared through this method, and also includes pharmaceutical compositions containing these effectors.

5           The present invention also includes a method of designing a specific inhibitor for a protein kinase, comprising the following steps: obtaining data regarding the three-dimensional structure of a first protein kinase, and using the data in the design of an inhibitor for a second, different, protein kinase. The first protein kinase is preferably cAMP dependent protein kinase or an analogue thereof. The obtaining step preferably  
10           comprises crystallizing a complex of cAMP dependent protein kinase and an inhibitor thereof, and additionally includes obtaining X-ray crystallography data on the crystallized complex obtained from the crystallizing step. Thus, information regarding the structure of the crystallized complex obtained in the crystallizing step through circular dichroism, small angle neutron scattering, or other chemical procedures can be obtained.

15           In a preferred form of the present invention, there is provided the use of the data of Figure 17 or of Table 4 in the design of an effector for a protein kinase.

          Still another aspect of the present invention involves a method of preparing a highly specific inhibitor of a first enzyme. The first enzyme is a member of a class of enzymes having a conserved catalytic core with a plurality of invariant residues. This method  
20           includes the following steps: (a) identifying a second enzyme that is a member of the class and having a known first inhibitor thereof, (b) forming a first complex of the second enzyme and the first inhibitor, (c) obtaining data regarding the three dimensional coordinates of the invariant residues in the first complex, (d) designing a second inhibitor which computer modelling indicates will induce a conformation on the catalytic core of the first enzyme in  
25           which the invariant residues are in substantially the same coordinates as the coordinates obtained in step (c), when the first enzyme is formed as a second complex with the second inhibitor, (e) preparing the second inhibitor, (f) forming a third complex of the second inhibitor and a third enzyme complexable therewith, the third enzyme having a plurality of the invariant residues, (g) obtaining data regarding the three dimensional coordinates of the  
30           invariant residues in the third complex, and (h) using the data obtained from step (g) to design a third inhibitor which computer modelling indicates will induce a conformation on the catalytic core of the first enzyme closer to that in which the invariant residues are in substantially the same coordinates as the coordinates obtained in step (c) than induced by the second inhibitor, when the first enzyme is formed as a fourth complex with the third



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inhibitor. This first inhibitor is in one embodiment of this method an inhibitory domain of the second enzyme. The third enzyme preferably contains at least 5 invariant residues, and can be a naturally occurring enzyme or a mutant enzyme.

5 Still another aspect of the present invention involves a method of determining the efficacy of a first effector in affecting a first enzyme that is a member of a class of enzymes having a plurality of invariant residues among the members of the class. This method includes the following steps: determining the three dimensional coordinates of the invariant residues of a second enzyme in a first conformation wherein the second enzyme is in a complex with a second effector that is a strong effector of the enzyme, determining the three  
10 dimensional coordinates of the invariant residues of the second enzyme in a second conformation wherein the enzyme is in a conformation other than the first conformation, identifying the mobile invariant residues of the enzyme, the mobile invariant residues being those invariant residues at coordinates substantially different in the first conformation than in the second conformation, determining the three dimensional coordinates of the mobile invariant residues of the first enzyme when the first enzyme is in a conformation wherein the first enzyme is in a complex with the first effector, comparing the three dimensional coordinates of the mobile invariant residues of the first enzyme in the conformation with the coordinates of the mobile invariant residues of the enzyme in the first conformation, wherein relatively small differences in the coordinates indicate relatively high efficacy of the  
15 first effector. The step of determining the coordinates of the first enzyme in the conformation is preferably performed using computer modelling of the conformation. The steps of determining the first and second conformations preferably comprise obtaining X-ray crystallographic data of the enzyme. The second conformation can be a conformation produced by a ternary complex, such as one comprising a protein kinase, a nucleotide and an effector. The second conformation can also be a conformation produced by the second  
20 enzyme not complexed with a ligand, or the same enzyme as the first enzyme.

25 In an additional aspect of the present invention, there is provided a method of designing specific inhibitors of a first protein kinase having a template defined by a plurality of invariant residues present in substantially all protein kinases. This method comprises the following steps: obtaining data regarding the three dimensional coordinates of the invariant residues of a second protein kinase and of the points of contact between the second protein kinase and a known inhibitor thereof, the coordinates being obtained when the second protein kinase is formed as a complex with the known inhibitor, generating a model of the first protein complex wherein the template is defined by the positions of the invariant  
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residues in the complex, examining the amino acid residues present in the first protein kinase at positions corresponding to the points of contact in the complex, and designing an inhibitor of the first protein kinase capable of forming ionic and hydrophobic interactions with the amino acid residues. The method of Claim 62, wherein the second protein kinase is cAMP dependent protein kinase. The known inhibitor can be PKI(5-24). For this known inhibitor, the points of contact in the complex preferably comprise positions corresponding to the positions selected from the group consisting of P+1, P-2, P-3, P-6 and P-11 along the known inhibitor. The positions corresponding to the points of contact in the examining step preferably comprise positions within a sphere having a radius of 11 Å, more preferably 6 Å, from the coordinates of the point of contact obtained in the obtaining step. The designing step preferably additionally comprises designing the inhibitor to form appropriate hydrogen bonding with the amino acid residues.

Further details concerning the present invention are provided in the following detailed description.

#### Detailed Description of the Invention

#### CITED REFERENCES INCORPORATED BY REFERENCE

A number of articles are specifically cited herein as providing background information useful, but not essential, to those of ordinary skill in the art in the practice of the present invention. As such, the disclosure of each of these articles is hereby explicitly incorporated by reference.

#### INTRODUCTION

The protein kinase family of enzymes is used as a model for this invention. These enzymes are involved at all levels of regulation in the eukaryotic cell. They act as "transistors" for the cell, receiving signals and amplifying the message inside the cell. Protein kinases receive hormone signals from outside the cell. They are involved in cell growth, for cellular homeostasis, and for triggering the steps of mitosis.

In addition, many oncogenes code for protein kinases. These oncogenic protein kinases are also very diverse in their structure and location within the cell. However, all are derived from normal cellular components and all, in one way or another are defective in their ability to be turned off. In other words, they are constitutively active in contrast to their protooncogene counterparts which are turned off in the absence of the appropriate signal. Thus, protein kinases are not only an essential part of normal cell growth and division, but, can lead to oncogenesis when their normal function becomes genetically impaired.

Diversity is a hallmark of the protein kinase family. For example, growth factor receptors, such as the insulin receptor, are large proteins with a major extracellular domain for binding growth factor, a single membrane spanning domain, and an intracellular protein kinase domain that is activated in response to growth factor binding. The kinase activity is limited to a specific domain of the protein. Control of the insulin receptor may play an important role in the control of diabetes. Protein kinase C is activated by diacyl glycerol and  $\text{Ca}^{2+}$  and is also activated by the tumor promoting phorbol esters. It is a cytoplasmic protein that in its active state is associated with the plasma membrane. Another protein kinase, cdc2, associates with cyclin B and is an essential trigger for mitosis. The transforming protein in Rous Sarcoma Virus, pp60<sup>v-src</sup> is anchored to the cytoplasm surface of membranes. In spite of the diversity in size, subunit composition, location in the cell, and mechanism of activation, all protein kinases share a common enzymatic activity and a conserved catalytic core, indicating that all have likely evolved from a common functional precursor. Thus, one aspect of the present invention provides a method for developing highly selective inhibitors for members of the protein kinase family.

The first protein kinase to be purified was phosphorylase kinase. The second was phosphorylase kinase kinase, later renamed cAMP-dependent protein kinase (EC2.7.1.37:ATP:protein serine phosphotransferase) when its broader substrate specificity was appreciated. Not only was cAMP-dependent protein kinase (cAPK) one of the first protein kinases to be characterized, it also is one of the simplest and best understood biochemically. Its simplicity is due primarily to its mechanism of activation, which involves subunit dissociation. With the exception of the oncogenic enzymes, all protein kinases typically are maintained in an inactive state in the absence of the appropriate activating signal. In the case of cAPK, the ligand triggering activation is cAMP, one of the first recognized second messengers for hormone signalling. In the absence of cAMP, the enzyme is sequestered as an inactive holoenzyme containing two regulatory (R) and two catalytic (C) subunits. When intracellular cAMP levels are elevated, the cyclic nucleotide binds to the R-subunit, thus causing the complex to dissociate into a  $\text{R}_2$  dimer and two free and active C-subunits. The general consensus sequence recognized by the C-subunit is Arg-Arg-X-Ser/Thr-Y, where X is any small residue and Y is a large hydrophobic group. The conserved catalytic core found in all protein kinases is contained within this relatively simple monomeric C-subunit.

This invention provides the first crystal structure of a protein kinase with its catalytic subunit intact. Knowledge of the conformation of the catalytic structure of cAPK is central

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to the understanding of protein kinase activity. Not only is the structure of the cAMP-dependent protein kinase catalytic site provided, but, the crystals contain a bound inhibitor peptide. This inhibitor peptide, PKI(5-24), is a fragment of the heat stable protein kinase inhibitor (PKI). This peptide includes the consensus features common to all peptide substrates and inhibitors of cAMP-dependent protein kinase. In addition, it contains other features that convey unique high affinity binding characteristics. Thus, precise properties of binding and interaction are described. From this data, a template is derived from which all other protein kinases can be modelled and from which other inhibitors can be designed.

One of the more important questions regarding protein phosphorylation is how the targeted protein substrate is recognized by a specific protein kinase. This question has remained particularly elusive until now because the determinants for peptide recognition are widely dispersed and in some cases well-removed from the actual site of phosphotransfer. Owing to its simplicity as well as its relative ease of purification, the catalytic or C-subunit of cAMP-dependent protein kinase serves here as a prototype for identifying functional sites that are involved in substrate recognition and catalysis. Chemical analyses and procedures, such as affinity labeling, group specific labeling, and fluorescence energy transfer all have provided clues about regions involved in peptide recognition, MgATP binding, and catalysis. Substrate analogues provide indirect information about binding sites important for effector molecule specificity. Further NMR, circular dichroism, small angle neutron scattering (SANS) and other chemical procedures offer further insight into the structure of the enzyme. However, X-ray crystallography provides a comprehensive three dimensional structure that can confirm and integrate these other techniques.

The expression of the C-subunit in *E. coli* not only facilitated these structural studies, but also has permitted recombinant approaches to be used to further modify the active site of cAPK and thereby mimic the reactive site of other protein kinases. Information to aid in these studies is obtained from sequence data available for the protein kinase family. Hanks et al., Science 241: 42, 1988, is one source of such data. Such sequence comparisons have identified highly conserved regions including several invariant residues, variable regions, and places where inserts and deletions can be tolerated. Both chemical and sequence information are used here to verify the structure data obtained from the X-ray diffraction studies. As will be disclosed herein, this body of information permits the design of other effector molecules specific for other protein kinases. Further, this information serves as guidelines for the design of specific effector molecules for enzymes from a wide variety of enzyme families.

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The existing basis for the design of specific inhibitors for protein kinases, in the absence of the three dimensional structure provided herein, relies on the use of synthetic peptides based primarily on the sequences of known substrates and inhibitors. In the case of cAMP-dependent protein kinase, there are some very specific high affinity peptides available. Existing inhibitors also include nucleotide and nucleoside derived compounds found through traditional means. However, these nucleoside and nucleotide inhibitors do not generally exhibit the type of specificity observed with peptide inhibitors. In general, such specific peptide inhibitors are not available for other protein kinases. Specificity for cAMP-dependent kinase improves with the addition of amino acids postulated to lie outside of the catalytic core. We have discovered that these regions are also important for inhibitor design. Knowledge of these sites provides a "lock" to permit for the first time the tailoring of inhibitors for any given protein kinase. Thus, one important aspect of the invention lies in the design of the "lock", that requires an understanding of the three dimensional structure of the complex of the catalytic subunit of cAMP-dependent protein kinase, with its very potent specific inhibitor, PKI(5-24).

Disclosed herein is a template gleaned from the crystal structure of the catalytic subunit of cAMP-dependent protein kinase. Just as the chemical information derived from the C-subunit serves as a framework for interpreting the entire kinase family, the structure of cAPK provides information for the creation of a template for viewing the conserved catalytic core of all eukaryotic protein kinases. This invention further provides a model for the identification and design of molecules capable of interacting with the catalytic core of a given enzyme by analyzing the conserved catalytic core of another member of that enzyme class.

#### X-RAY CRYSTALLOGRAPHY

X-ray crystallography permits three dimensional molecular analysis of a protein at the atomic level. Analysis requires the production of crystals and crystal production requires a pure concentrated product. Further, complexes of a protein of interest together with a second interacting molecule provides information on the conformational changes occurring within a protein in response to that second molecule. X-ray crystallography of a protein with its substrate, an antibody or a drug can provide information for rational drug design.

An X-ray diffraction pattern taken from a crystal looks like an array of spots of varying intensities. Each spot is related to one of the Fourier coefficients of the electron density pattern in the crystal. Thus, the electron density in the crystal can be reconstructed if a sufficient number of diffraction spots can be measured and the relative phase angles of

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the Fourier coefficients can be determined. Thus, a crystallized enzyme used in the practice of certain aspects of the present invention should be of sufficient quality to obtain these measurements. For example, the spots of varying intensity in the diffraction pattern decay over time. It is quite difficult to work with diffraction patterns with half lives of less than 10 hours. However, it is possible to work with diffraction patterns having half lives as short as about 15 minutes to 3 hours, depending on the amount of structural data desired to be obtained. Further, it is believed possible to work with crystals of even shorter half lives using equipment and computer programs more advanced than commonly available today. Additionally, not all crystals are of equal quality and poor crystals have large Bragg spacing diffraction limits. Thus, a workable crystal should have a Bragg spacing diffraction limit of less than 4 Å.

Determination of phase angles uses isomorphous replacement to insert atoms into defined positions in the crystal for diffraction data measurement. These angles provide information that permit the production of an electron density map. The map is then used to build an atomic model from which three-dimensional coordinates are measured that define the structure of the crystallized molecule.

#### MODEL SYSTEM

X-ray crystallography has been employed for the rational design of drugs and other interacting molecules. However, to date, the rational design of effector molecules has been limited to a study of the active site of the protein/effector molecule interaction. Potential effectors designed from this information have not been obtained by looking at interactions beyond the active site. We believe that these interactions assist in binding and thereby contribute to binding specificity. Thus, we have discovered that it is these interactions in concert with information obtained from the active site that make the design of specific effector molecules a possibility. Moreover, this information additionally permits the design of specific effector molecules for related but nonidentical enzymes.

Many enzymes within a cell have evolved from common progenitors. These enzymes share common enzymatic activities and one example is the protein kinase family. Since the functions of the enzymatic families or classes are broadly conserved, at least a portion of the catalytic site is also conserved. Therefore to a large extent rational drug design relies on the identification of the familial similarities and hence drugs are designed to react broadly within a given family or class.

While all members of an enzymatic class may provide a similar activity, such as phosphorylation or dephosphorylation, each member may have only one specific target.



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Thus, successful rational drug design based on group similarities would provide molecules that also interact broadly. Where there are many members of an enzymatic class acting specifically within a restricted locale such as a single cell, a broadly acting drug would interact with any number of enzymes from the group. Thus, the interaction would be general and not specific. In contrast, the present invention advantageously is capable of providing effectors with highly specific interactions for a given member of an enzyme class.

Previous methods for rational drug design require the crystallization of the target molecule of interest. However, the production of useful crystals is both difficult and time consuming. It first depends on the ability of the target molecule to be isolated and purified in sufficient quantity for crystallization. A large number of crystallization conditions often need to be tested and once a crystal is made that is of sufficient quality, additional crystals often need to be produced in order to have enough material for analysis. Further, not all molecules are readily purified or readily crystallized. Advantageously, the present invention discloses a method whereby only one enzyme within a family of enzymes need be crystallized.

This invention teaches a method for the identification and design of specific molecules interacting with a specific enzyme wherein the specific enzyme is a member of a broadly acting enzymatic group or class.

The particular enzyme class chosen for this invention is preferably one that has the characteristics generally associated with an enzyme class developed from a divergent evolutionary pathway. That is, an enzyme class in which it is possible to identify similarities within the catalytic core of all members of the class. Enzymes with similar activities that have evolved from convergent evolution will not necessarily share these constant residues and a model or template employing invariant amino acids as anchors would then not be possible. A variety of enzyme families are postulated to arise from divergent evolution, and thus would be expected to serve as a preferred class of enzymes for design of effector molecules within the context of the present invention. Such enzyme families include, but are not limited to, the protein kinases, phosphorylases, and several groups of proteases.

For purposes of illustration only, the present invention is described using the protein kinase family as a model system. As discussed above, these enzymes are essential for many aspects of cell regulation. Over 100 individual protein kinases have been identified. Thus, the successful design of effectors to manipulate the activity of a kinase can provide an invaluable tool for research as well as for the design of a wide variety of therapeutics and diagnostics.



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Thus, for example, development of effective specific inhibitors of oncogenic kinases is believed to lead to the development of anti-neoplastic treatments. In addition, specific inhibitors of kinases involved in hormone regulation will be useful in artificially regulating the secretion and regulation of such hormones. Also, since many neuro-transmitters are regulated by kinases, development of new effectors could potentially impact on diseases of the nervous system. Further, platelet aggregation and clot formation might also be regulated through novel effectors of kinases developed through the methods of the present invention. Many other therapeutics are believed possible through the development of novel specific effector molecules.

The model system used in connection with this invention uses cAMP-dependent protein kinase together with a 20 amino acid inhibitor peptide, PKI(5-24), to establish a "lock" for specific effector design. This inhibitor is unique in that it interacts only with the cAMP-dependent protein kinase. Therefore, cocrystallization of this inhibitor with cAMP-dependent protein kinase permits the visualization of the conformation of an enzyme in association with its specific inhibitor.

The general requirements for peptide recognition by the catalytic subunit were characterized originally using synthetic peptides. From those studies evolved a general consensus sequence that includes two basic residues, typically arginine, followed by one intervening small residue preceding the site of phosphotransfer. The phosphate acceptor site, either Ser or Thr, is followed immediately by a large hydrophobic residue. The typical peptide substrate used for this kinase, based on the phosphorylation site in pyruvate kinase, is shown in 1. Replacement of the Ser with an Ala generates an inhibitor peptide with poor affinity. In contrast is the inhibitor peptide, PKI(5-24), derived from the thermostable protein kinase inhibitor (PKI). This peptide, seen in 1, encompasses the consensus sequences described above but also contains additional unique features that convey high affinity binding. The particular features that contribute to high affinity binding were defined using peptide analogues, and the most relevant ones are also indicated in 1. A general structure of the peptide in solution was deduced using circular dichroism (CD) and NMR spectroscopy. The peptide, PKI(5-24), was co-crystallized with the catalytic subunit of cAPK, and the structure of that peptide as well as its interaction with the protein are discussed here.

The folding of the polypeptide chain and the mechanism of catalysis is conserved in all protein kinases. There are 8-9 invariant residues scattered throughout the core for all protein kinases. The crystal structure reveals that most of these invariant residues are

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clustered three dimensionally around the site of catalysis providing an interconnected network. The regions involved in peptide recognition extend over a wide area on the surface of the enzyme and until this structure was solved there was no understanding of the details of the peptide recognition sites. The structure of the catalytic subunit thus serves as a framework from which a template for the entire protein kinases family can be produced. This structure provides, for the first time, a true molecular basis for the design of effectors that will selectively target any given protein kinase. Thus, it is an object of this invention to provide a method for the identification and design of molecules interacting with the catalytic core of a protein kinase by preparing a template from the analysis of the catalytic core of the cAMP dependent protein kinase.

The ability to design effector molecules that act on a given enzyme using information obtained by X-ray crystallography is dependent on the formation of crystals of purified enzyme. Methods for crystal production vary greatly and one cannot predict how readily a given molecule or complex will crystallize. However, those skilled in the art will recognize that a variety of methods for crystallizing can be attempted for any given enzyme, and that successful crystallization can be expected of a variety of enzymes. Rational drug design additionally requires information about the interaction of a known effector in order to accurately predict a potential effector's effect on the catalytic core of the enzyme. Thus, crystals of the complex of effector molecule and enzyme together are used to gather information on the conformation of the enzyme in its inhibited conformation. Thus, in addition to information about the catalytic core of an enzyme family and the identification of additional sites adjacent to the core that permit the specific design of inhibitors, the present invention provides an improved method for the crystallization of complexes.

An important feature of certain aspects of this invention is the production of an enzyme/effector template. In order to generate this template, the effector chosen for production of enzyme/effector complex should have a high affinity for a particular enzyme. The initial effector molecule chosen should preferably have a  $K_d$  less than 1  $\mu M$ , and more preferably less than 100 nM, in order to provide a conformation resulting from high affinity interactions. Once the specific interactions are understood it is contemplated that effector molecules having a variety of  $K_d$  ranges could be selectively designed for various purposes. Thus, in the model system chosen to illustrate this invention, PKI(5-24) is used as an effector of cAPK, with a  $K_d$  of approximately 60 nM. Those of ordinary skill in the art will recognize that other inhibitors with  $K_d$  less than 100 nM could also have been chosen to illustrate this aspect of the present invention.

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For example, cGMP dependent protein kinase has an inhibitor with a  $K_i$  of approximately 6 nM, and an inhibitor for cAPK described by Ricouart et al. is characterized in the 4 nM range (J. Med. Chem., 34: 73-78, 1991). These  $K_i$  values are roughly equivalent, however, not identical, to the expected dissociation constants ( $K_d$ 's).

5       The PKI(5-24) inhibitor peptide used here is highly specific and is rather large in that it extends beyond the catalytic core. Other known peptides and effector molecules for kinases are not as specific. We have discovered that the interactions beyond the catalytic core provide the high specificity of PKI(5-24) for cAPK.

10       As stated above, it is the crystallization of the enzyme with its specific inhibitor together with the analysis of the relationship of the inhibitor to both the catalytic core and to areas surrounding the core that provide data for the particular protein kinase "lock". The "lock" comprises the three dimensional structure and ionic, hydrophobic, hydrogen bonding and other interactions of the non-conserved variable residues with the specific effector structure. The lock is defined by the invariant residues of the exemplary structure. When  
15       an enzyme of the class is affected by a specific effector, the backbone atoms of these invariant residues must be in substantially the same relative coordinates in all members of the enzyme class. Thus, with knowledge of sequence information of the particular enzyme for which the effector is being designed, knowledge of the lock formed by the invariant residues can be obtained. The coordinates of the invariant residues position the variable  
20       residues of the lock in space and thereby permits the design of other specific inhibitors and effector molecules for other protein kinases.

      The lock consists of the site of phosphotransfer (P site) with recognition sites for flanking sequences. The flanking sites can be identified by the number of amino acid residues separating that site from the P site. Thus, the first amino acid residue in the  
25       direction moving toward the carboxy terminus is designated P+1, and the following residues are designated P+2, P+3, P+4 and so on. Similarly the residues on the side moving toward the amino terminus are designated P-1, P-2 and so on.

      The sites for recognition of the peptide are not identical between members of the protein kinase family, and the chemical content is unique for each given protein kinase. The  
30       sequence of the given protein kinase is built into the coordinates of the C-subunit using the invariant residues. The position of these invariant residues can be identified using X-ray crystallographic data, such as the data disclosed herein in Figure 17. This data provides the coordinates for each non-hydrogen atom in cAPK. It is the locations of these invariant residues which serve to define the template common to all protein kinases. This template

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can then be used to model the three dimensional coordinates of the variable as a basis to design highly specific effector molecules.

5 The effector molecules to be designed could be polypeptides, nucleic acids and their analogues, combinations of nucleotides and peptides, organics or any other molecule capable of specific interaction with a given enzyme. The essence of the design of a specific inhibitor for a given protein kinase is based on the three-dimensional fit of the specific inhibitor into the provided "lock", or template, provided by the known structure of cAPK.

10 The template defined by the invariant or other highly conserved residues can be used to define the region immediately flanking the phosphorylation site and, in addition, can incorporate more distant parts of the molecule to enhance specificity and affinity. The peptide recognition site serves in the same manner as the antigen recognition site of an antibody. This site extends over a large surface of the enzyme and provides a unique lock for the design of a wide variety of effector molecules, including both peptide and non-peptide effectors. Each particular protein kinase has a different and unique chemical content at each individual site. Thus, the "lock", is unique for each protein kinase.

15 The "lock" of any particular enzyme represents a topological map with defined sites, positions of which vary between members of the enzyme class. As an analogy, each kinase can be thought of as functioning in a manner similar to a specific antibody in that it recognizes only a very specific set of proteins to phosphorylate. However, each of the kinases has a conserved template, the positions of which will not substantially vary between kinases in an inhibited conformation. Thus, using computer modelling together with known sequence information regarding a particular kinase, the invariant residues of the kinase can be placed in the template conformation, and the approximate positions of the variable residues can be predicted.

25 The lock provides the information from which other specific effector molecules can be designed. It provides information on topology, charge interactions and the points of contact both within the catalytic core and around the core that suggest the design features important for the production or identification of novel effector molecules. Thus, the goal is to design an effector having homologous topography and charge fields that complement the catalytic core of the lock of the enzyme. Computer modelling can be used with these factors to design an effector capable of inducing a conformation where the conserved amino acid residues of the enzyme are in homologous locations to the template.

#### BRIEF DESCRIPTION OF EFFECTOR DESIGN

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The basic steps toward achieving this invention are provided briefly here and in detail below. A class of enzymes is first identified wherein at least one enzyme of the class has a highly specific affector molecule. Then the inhibitor is tested for specificity and, preferably, the inhibitor sequence is reduced in size until a minimum sequence having the desired specificity is obtained. Sequence data from related enzymes is analyzed so that a consensus region that forms the catalytic core can be identified. Crystals of affector molecule together with the model enzyme are subjected to multiple isomorphous replacement techniques to prepare heavy atom derivatives. This permits the location of heavy atoms within the structure to be identified and additionally permits multiple diffraction patterns to be combined to deduce phase angles for calculation of the electron density of the structure. Those of ordinary skill in the art will recognize that other techniques can be used to deduce phase angles and to improve the accuracy of previously deduced phase angles.

A three-dimensional structure can be obtained from the electron density data using a computer program such as TOM/FRODO. Further, a computer program, such as X-PLOR, can be used to improve the accuracy of the initial three-dimensional structure. There are a variety of computer programs available for analyzing X-ray crystallographic data. Those used in the development of the model system for this invention are cited herein. Those of ordinary skill in the art will recognize that many other such computer programs providing similar functions could also have been used. From this data, the points of contact are identified both within the catalytic core and the surrounding region. Invariant amino acids and consensus recognition sequences are identified. The data is further analyzed against available chemical data such as NMR, CD, SANS data and other data resulting from chemical procedures. This chemical data can provide additional information for the structural model.

The coordinates of the invariant amino acids residing in the conserved catalytic core and the surrounding invariant residues in the enzyme/affector complex provide the template to be duplicated in other members of the enzyme class. The lock of the enzyme for which the affector is to be designed is then built by replacing the variable amino acids of the catalytic subunit of the template enzyme with the amino acids of the new enzyme. Any gaps in the sequence alignment between the enzyme used to generate the template and the enzyme for which the lock is being modelled generally occur within loops. These loop regions can be modelled separately using the structural data accumulated in a data bank, such as the Brookhaven data bank. The model of protein kinase can then be corrected and



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refined using an energy minimization procedure and using molecular dynamics to eliminate steric and electrostatic clashes. The resulting model of the catalytic core of the protein kinase under investigation is then inspected for amino acid content of the enzyme's surface which interacts with the proposed inhibitor.

5 In accordance with one aspect of the present invention, another member of this enzymatic class can then be analyzed in the context of this template. If the new enzyme can be crystallized, then the information obtained from the crystallization is merged with the "lock" structure. However if the new enzyme is not accessible or is not crystallizable, the enzyme can still be incorporated into the three-dimensional lock. The ability to incorporate  
10 the new enzyme into the template is dependent on the identification of conserved residues within the catalytic core of the new enzyme that are complementary to the conserved residues in the model enzyme. The template establishes the coordinates for these residues in three-dimensional space as well as providing coordinates for the three-dimensional surface of the catalytic core and adjacent regions.

15 For cAPK and the protein kinase family, the invariant residues are identified and summarized in the review by Hanks et al., supra. The template permits a comparison of the new enzyme catalytic core surface with cAPK. Residues within the catalytic core that are different from those of cAPK are studied to determine how those differences in the new enzyme might alter the surface of the core or change the structure of a new effector  
20 molecule. Recombinant cAPK can then be subjected to site-directed mutagenesis to change residues specific to cAPK into residues found in the new enzyme. This recombinant protein can be crystallized.

A novel effector molecule can then be synthesized that complements the electrostatic charges and topography of both the catalytic core and identified surrounding regions of  
25 interest for the new enzyme. The points of contact, hydrophobic pockets, site of phosphotransfer, topography and steric interactions are assessed and the effector molecule can then, if necessary, be subjected to random mutagenesis or site-directed mutagenesis to improve the effector/enzyme interaction. This model effector molecule together with recombinant mutated cAPK, are tested with the target enzyme for effector activity. The  
30 effector molecule is finally tested with the native new enzyme. Fluorescent tags bound to the effector can be used to assess binding to the new enzyme in the cell. Alterations in enzyme function can be detected by gel electrophoresis and complexes of enzyme and effector can be isolated and purified for further analysis. Thus, new enzyme purification and crystallization is not required for effector design.



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As discussed above, generation of new effectors is not limited to peptides. A variety of chemically synthesizable compounds can be used.

The model can be tested by a variety of methods. For example, kinetic determination of inhibition constants of novel inhibitors can be measured. Also, CD, SANS and other chemical procedures can be used to assess the extent of the conformation changes due to binding of the effector. If a mutated form of the enzyme has been prepared, cocrystallization of the effector with this mutated form can be performed and the points of contact can be determined and compared with the modelled points of contact.

#### ENZYME FAMILY CHOICE AND IDENTIFICATION OF CATALYTIC CORE

This invention relates particularly to enzyme families formed by divergent evolution. Once an enzyme family of interest is identified, an individual enzyme is chosen from a group of enzymes that share invariant residues within their postulated active sites.

The enzymatic or active site within a given protein kinase can be broadly identified through biochemical means. When the enzyme exists as a group of subunits, enzymatic activity is often restricted to one of those subunits. Thus, prior to performing these biochemical means, the enzymatic subunit can be purified from the holoenzyme. The active site can be further localized by systematically reducing the subunit size and assessing enzyme activity with each reduction. In one method, the various mRNA sequences encoding the related enzymes are reversely transcribed and cloned. Sequence information can then be obtained from the catalytic region for a number of enzymes of the same class. Similar amino acid residues within the catalytic subunit are aligned in order to visualize homologous regions. Invariant amino residues can be identified among the class which are either present in all known members of the class or substantially all members of the class. At least a plurality of these invariant residues are believed necessary for enzyme activity within the catalytic subunit. Thus, the invariant residues can further define the catalytic core.

For the protein kinase family, invariant amino acid residues are located within the catalytic core and are boxed in by a solid line in Figure 1. Figure 1 illustrates the general topological arrangement of the catalytic subunits from a number of protein kinases.

Figure 2 illustrates that while the catalytic regions from members of the protein kinase family share some striking similarities, the placement of this active region within the enzyme, the size of the enzyme and the regulatory regions of the enzyme vary considerably. The conserved catalytic core is denoted in Figure 2 as solid black areas and regulatory regions are cross-hatched. Additional information regarding the use of cAMP-dependent

Protein Kinase as a model for the protein kinase family can be found in a review by S. Taylor (J. Biol. Chem. 264:8443-8446, 1989.).

5 It is known from an analysis of the catalytic core of the protein kinase family that the core is included in a conserved 300-residue segment. Site-directed mutagenesis of recombinant enzyme sequences has been used to identify particular residues critical to enzymatic function. In the cAMP-dependent kinase an invariant lysine residue at position 72 has been shown to be important by site-directed mutagenesis and a triad of glycines is thought to be associated with ATP-binding.

10 The enzyme exists as a tetrameric holoenzyme composed of a dimer of regulatory subunits and two catalytic subunits. cAMP binds to the regulatory dimer yielding dissociation of the enzyme into an  $R_2(cAMP)_4$  complex and two active catalytic (C) subunits. It is the active C-subunit that phosphorylates serine or threonine residues on substrates having the consensus sequence Arg-Arg-X-Ser/Thr-Leu.

#### AFFECTOR MOLECULE FOR TEMPLATE DEVELOPMENT

15 In a preferred form of the present invention, the enzyme used to establish the template or lock is, advantageously, a molecule that binds with high affinity to its effector, preferably with a dissociation constant less than 1  $\mu$ M. For example, there are many such known effectors, such as inhibitors and activators, of various protein kinases. Kinases with a regulatory subunit are known that are inhibited by a peptide encoding the regulatory subunit binding site. Similarly, kinases that possess an autoinhibitory portion are also  
20 known. Thus, for such a kinase, this autoinhibitory region could be cleaved away from the core enzyme, purified and analyzed to provide a minimal high-affinity inhibitory sequence.

There are several inhibitors of cAMP-dependent kinase. The regulatory subunits can function as physiologic inhibitors as can the heat stable inhibitor protein (PKI). These  
25 inhibitors share a substrate-like sequence based on the arginine doublet, N-terminal to the position of the phosphorylation site in a normal substrate. Peptide fragments containing the consensus sequence bind the C-subunit in a manner analogous to a real substrate. PKI has an alanine in place of the phosphorylatable residue. While the PKI sequence is clearly inhibitory, the addition of a 15 residue stretch N-terminal to PKI increases inhibitory  
30 activity. Thus, residues external to the catalytic site are believed to be relevant in providing potent, high-affinity, inhibition and for improving the specificity of an inhibitor.

A protein that is a high-affinity inhibitor of an enzyme can be dissected to find a smaller fragment, if it exists, that still contains high-affinity inhibitory activity. At least three factors are useful in this dissection: 1) an ability to produce chemically defined fragments

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of the larger inhibitor, either by synthesizing peptides or by cleaving the inhibitor with reagents such as cyanogen bromide or proteases, that cut at short amino acid sequences of a specific type for each reagent, 2) an ability to isolate specific fragments of the larger inhibitor from the mixture of fragments resulting from cleavage of the larger inhibitor, and  
5 3) an ability to assay chemical species for inhibition of the enzyme of interest.

To carry out the isolation of a potential smaller inhibitory region of a larger inhibitor, one can cleave the inhibitor into fragments using a protease. Then one can separate the resulting fragments using HPLC and assay the fractions for high-affinity inhibition of the target enzyme. If no fraction is found that exhibits the desired inhibition,  
10 the cleaving reagent may have cleaved at a location that splits the inhibitory portion of the protein, destroying its ability to inhibit. In this case, it would be desirable to obtain other cleavage patterns until an inhibitory fragment is found. After obtaining the smallest possible inhibitory fragment using proteolytic cleavage of the intact inhibitor, one can chemically sequence the fragment as a step toward further defining the smallest fragment still having  
15 high-affinity inhibitory activity. With knowledge of the amino acid sequence, one can then use peptide synthesis to construct progressively shorter subsets of this fragment. These shorter subsets can then be assayed for inhibitory activity. Proceeding in this manner will thus allow definition of the smallest sequence, present in the larger inhibitor that still possesses high-affinity inhibitory activity toward the target enzyme. Methods for  
20 determining inhibition constants for tight-binding inhibitors are found in Biochem. J. 127: 321-333, 1972 by P. Henderson. Methods for determining the inhibitory region PKI(5-24), are provided by Scott et al. in Proc. Natl Acad. Sci. USA 82:4379-4383, 1985.

#### OBTAINING THREE DIMENSIONAL STRUCTURE DATA

In order to obtain data on the conformation of the template of the enzyme formed  
25 by binding of the effector thereto, a variety of techniques can be used. These techniques include, circular dichroism, small angle neutron scattering, diffraction methods, including any combination of multiple and single isomorphous replacement, single or multiwavelength anomalous scattering methods, molecular replacement methods maximum entropy phasing, solvent-flattening methods and so-called "direct" methods used primarily to solve small-  
30 molecule structures. However, in the preferred embodiment, X-ray crystallography is used in order to generate specific coordinates for each of the non-hydrogen atoms in the complex. Coordinates for the hydrogen atoms could additionally be obtained using neutrons. Thus, following the isolation of an exemplary protein and effector and following or during the sequence analysis of related enzymes, crystals of enzyme and effector protein are generated.

The crystals can be generated from enzyme purified from natural tissue or from enzyme generated by recombinant means. Provided below are examples pertaining to the production of crystals using the recombinant mouse  $C_{\alpha}$ -subunit of cAMP dependent protein kinase and purified cAMP-dependent protein kinase from porcine heart. Nelson et al. describe the purification schemes for porcine heart cAMP dependent kinase (J. Biol. Chem. 256:3743, 1981.) and Slice et al. disclose the methods for the generation of recombinant mouse  $C_{\alpha}$ -subunit in E. coli (J. Biol. Chem. 264:20940, 1989). The sequence data for cAPK was published by Uhler et al. (J. Biol. Chem. 261:15360-15363, 1986).

The steady state kinetics of the C-subunit, purified from E. coli are identical to the mammalian C-subunit, although the E. coli protein is more labile to heat denaturation. Unlike the mammalian enzyme, the recombinant C-subunit lacks a myristoyl group at its amino terminus. For a review of protein crystallography see Protein Crystallography, 1976, T. Blundell and L.N. Johnson, Academic Press, New York. Information on circular dichroism and neutron scattering is found in Biophysical Chemistry. Part II: Techniques for the Study of Biological Structure and Function, C.R. Cantor et al. (W.H. Freeman and Co., San Francisco, 1980).

#### Example 1

##### Porcine Heart C-subunit Crystal Forms

Reagents were obtained from the following sources: threo-1, 4-dimercapto-2,3-butanediol (DTT, dithiothreitol; Aldrich, Milwaukee, WI); N,N-bis(2-hydroxyethyl)glycine (Bicine; Aldrich); methanol (Fisher Scientific); ammonium acetate (Aldrich); polyethylene glycol (Dow, Midland, MI).

The peptide inhibitor PKI(5-24) was synthesized at the La Jolla Cancer Research Foundation (La Jolla, CA) and modified in our laboratory. These modifications are described in detail below. The sequences of the peptide inhibitors are: (1)PKI(5-24); TTYADFIASGRTGRRNAIHD, (2)PKI(5-24), tyrosine iodinated: TTY\*ADFIASGRTGRRNAIHD. The peptide sequence abbreviations follow either of the two standard abbreviation schemes for amino acids; the three letter code or the single capital letter designation. Both are standard abbreviations and are well understood by those of skill in the art.

The porcine C-subunit was purified to a single band on SDS-polyacrylamide gels and used for crystallization. Two crystal forms were prepared. Photographs of the porcine heart apoenzyme (cubic); and the porcine heart C:MgATP:PKI(5-24) ternary complex (hexagonal) are provided as Figures 18A and 18B.

The first crystal form used the hanging-drop vapor diffusion method. A drop of protein mixed with precipitating agents is suspended from a microscope cover slip and allowed to equilibrate through the gas phase against a larger reservoir.

Specifically, 30- $\mu$ L drops of 3-4 mg/mL protein solution were suspended and allowed to equilibrate against approximately 1mL of reservoir solution in wells of plastic Linbro tissue culture trays over a time of several days to weeks. Both new forms, as well as the earlier P2<sub>1</sub> form, were grown at 4°C. The porcine heart C-subunit was concentrated to 8-12 mg/mL and subjected to a final dialysis before attempting crystallization. The specific recipe for obtaining the first new form was the following: drop- 1/3 protein in 50 mM (NH<sub>4</sub>)<sub>2</sub>HPO<sub>4</sub> and 5 mM 2-mercaptoethanol (pH 8.0-8.2); 1/3 150 mM NH<sub>4</sub>CH<sub>3</sub>COO, 50 mM (NH<sub>4</sub>)<sub>2</sub>HPO<sub>4</sub>, and 10 mM dithiothreitol (DTT) (pH 8.1-8.2); and 1/3 reservoir composed of 8-9% PEG-400, 17-20% MeOH, and 10 mM DTT. Crystals of the second form were obtained from the same conditions as the first new form when the drop contained, in addition to the protein, MgATP and a 20-residue peptide inhibitor [PKI(5-24)] in the molar ratio 20:5:1:1 ATP:Mg<sup>2+</sup>:PKI(5-24):C-subunit. The same crystal form was subsequently grown from a drop containing 1/3 protein in 50 mM bicine, 100 mM NH<sub>4</sub>CH<sub>3</sub>COO, and 5 mM 2-mercaptoethanol (pH 8.3); 1/3 MgATP and PKI(5-24) in 10 mM DTT in the same ratio to protein as before; and 1/3 8 mM DTT and 8% PEG-400. The reservoir contained 8% PEG-400, 15-20% MeOH and 7mM DTT. The first new crystal form could also be grown in the presence of the Mg<sup>2+</sup> and the non-hydrolyzable ATP analogue adenosine 5'β, γ-methylenetriphosphate (AMP-PCP). The second new crystal form, representing the ternary complex, could be grown with CoCl<sub>2</sub> or CdCl<sub>2</sub> substituted for MgCl<sub>2</sub> in the crystallization. The transition from one crystal form to another caused only by addition of MgATP and the peptide inhibitor PKI(5-24) suggests that a significant conformation change may occur upon their binding.

The space groups of the new crystal forms were determined to be P4<sub>1</sub>32 (cubic) (Figure 18A), and P6<sub>1</sub>22 (hexagonal) (Figure 18B), respectively. Space groups were determined and all diffraction data were measured at the University of California, San Diego Research Resource Laboratory at 4°C using graphite-monochromated CuK<sub>α</sub> X-rays from either the Mark II Elliot GX-6 rotating anode diffractometer operating at 2 kilowatts or the Mark III Rigaku RU-200 rotating anode diffractometer (available from Rigaku USA, Danvers, MA) operating at 5 kilowatts, each equipped with two Xuong-Hamlin multiwire area detectors (available from San Diego Multiwire Systems, San Diego, CA).



Preferably, area detector data collection is used. One facility offering equipment to support this data collection technique is The Resource Research Laboratory. This facility is a geographically designated, NIH supported facility to promote the use of X-ray crystallographic techniques. In speed, signal-to-noise ratio, and data precision, area detector data collection far surpasses standard diffractometer or film data collection. On the average, data collection is 50 times faster; consequently complete high resolution data sets can frequently be collected from a single crystal in one or two days. The space groups and lattice constraints of the crystal forms were determined to be the following:  $P4_132$ ,  $a=b=c=169.24 \text{ \AA}$ ; and  $P6_122$ ,  $a=b=80.3 \text{ \AA}$ ,  $c=293.0 \text{ \AA}$ . Calculations using an average reciprocal density of  $2.7 \text{ \AA}^3/\text{D}$  yield to the nearest unit 2 and 1 C-subunit monomers/asymmetric unit. The  $P4_132$  form diffracts typically to  $3.2 \text{ \AA}$ . Pictures of the cubic and hexagonal crystal forms can be seen in Figure 18

Because the  $P6_122$  crystal form had diffraction better in extent and decay characteristics than the  $P4_132$  form and because of the greater biochemical interest of a ternary complex, work concentrated on solving the hexagonal ternary complex crystal form. The lack of phase angles for a similar protein structure prohibited an initial structure solution for the C-subunit in the  $P6_122$  form using molecular replacement techniques, so a structure solution using standard multiple isomorphous replacement (MIR) techniques was attempted. Both of these are techniques known to those of ordinary skill in this art. Briefly MIR involves introduction into the space group asymmetric unit of a relatively heavy reference atom that, after being located through difference Patterson analysis, enables the needed phase angles to be determined. The reference atom can be found with  $6\text{-\AA}$  data, and with its location and generation of phase angles the fundamental crystallographic problem of a protein structure solution is solved and an electron density map can be calculated. Subsequent work on a protein structure focuses on incrementally improving the degree of detail visible in the electron density map through acquisition of higher resolution data and accompanying phase angles.

The procedure used to search for heavy-atom derivatives was to soak or co-crystallize C-subunit with heavy atoms based on the empirical success record or various heavy atom reagents and on known C-subunit chemical information, such as the availability of two free thiol groups and the obligatory use of a divalent cation in catalysis. Soaks in Au, Hg, and Pt compounds yielded precession picture diffraction changes but uninterpretable  $6\text{\AA}$  difference Patterson maps. A  $4.8\text{-\AA}$  data set from a  $\text{Na}_2\text{U}_2\text{O}_7$  soak yielded an apparent Patterson solution through examination of isomorphous difference and  $(1/\text{variance})$ -



weighted anomalous difference Patterson maps, but the site quality was not high and attempts to reproduce or improve the soak failed. Isomorphous crystals grown with  $\text{Co}^{2+}$  or  $\text{Cd}^{2+}$  substituted for  $\text{Mg}^{2+}$  proved useless since neither metal could be located (location of  $\text{Co}^{2+}$  through Patterson analysis was improbable anyway due to its lightness), although with phases their positions could reveal metal site number and location.  $\text{Co}^{2+}$  and  $\text{Cd}^{2+}$  were chosen for co-crystallization based on their reported ability to support nucleotide binding to the C-subunit and support catalysis, although at a reduced rate.

The single most important modification in the crystallization protocol that led to the formation of crystals in a different space group was the careful selection of polyethylene glycol in combination with various low molecular-weight alcohols. Commercially available polyethylene glycol contains various contaminants that may cause problems in the achievement of stable and reproducible crystallization conditions. All commercially available polyethylene glycols (PEG) were examined with the aim of detecting the presence of ionic species.

The lowest level of ionic contaminants was detected in PEG manufactured by Dow Chemical. It is this PEG that was selected for further crystallization experiments. PEG from other sources appeared to be generally more contaminated and also exhibited large differences in contamination between batches. In our experiments, several molecular weights of PEG were used along with several low-molecular-weight alcohols.

The catalytic subunit crystallized in the hexagonal space group with the introduction of PKI(5-24) and MgATP, whereas in its apo form it crystallized in the cubic space group using otherwise identical crystallization conditions, indicates that the hexagonal crystal may arise as a result of a different conformational state of the enzyme.

### Example 2

#### Mouse recombinant C-subunit Crystal Forms

One of the most promising directions for combining crystallographic methods with those of molecular biology is the development of highly effective vectors for expressing large amounts of protein for crystallization. Expression of protein in *E. coli* also provides a mechanism for eliminating posttranslational modifications which may hinder crystallization and in addition permits structure-function studies on mutant forms of the protein following the generation of mutant containing crystals.

The recombinant murine catalytic subunit, whose expression and purification was described by Slice et al., is devoid of myristic acid at the N terminus and differs by nine amino acids from the porcine heart catalytic subunit used in the earlier crystallizations. It

has been shown, however, that N-terminal myristoylation is not necessary for C-subunit function. Additional differences between the porcine heart and recombinant mouse  $C_\alpha$  proteins include the presence of additional phosphorylation sites (Ser 10 and Ser 139) on the recombinant protein.

5 Crystals were prepared from a binary complex of the recombinant mouse  $C_\alpha$ -subunit with a bound, high-affinity ( $K_i = 3$  nM) inhibitor peptide. The peptide (PKI95-24) derived from the N-terminal region of the naturally occurring thermostable protein kinase inhibitor protein (PKI), is the same peptide inhibitor used for the porcine heart ternary complex crystal. The steady state kinetics of the C-subunit purified from E.coli, are indistinguishable  
10 from those of the mammalian C-subunit, although the E. coli protein is more labile to heat denaturation.

The recombinant protein was crystallized using a small variation of the porcine heart ternary complex (hexagonal) conditions. A photograph of an exemplary crystal is provided in Figure 18C. First a ternary complex was prepared with MgATP and PKI(5-24). A  
15 C:PKI(5-24) binary complex was obtained after small-angle neutron scattering experiments showed that for the recombinant mouse C-subunit, the PKI(5-24) peptide alone, without MgATP, was able to cause a significant decrease in the radius of gyration. The ternary complex crystal form diffracted to at least 2.7 Å on the Mark III and was of orthorhombic space  $P2_1^2 2_1^2$ . A data collection strategy following the procedure of Xuong, et al., (Acta  
20 Cryst. B41: 267, 1985) was developed. Equipment for use with this procedure is available from San Diego Multiwire Systems of San Diego, California. The procedure allowed an asymmetric unit of data to be collected in 3  $\omega$ -sweeps totaling about 140° (with appropriate choice of  $\phi$  and  $\chi$  settings and a crystal mounted with one of the axes parallel to the capillary axis). Data collection took about 16 h for a >90% complete 2.7-Å data set from one crystal  
25 with  $R_{sym}$  on the intensity of 4-6%; in the same period the average reflection intensity decayed approximately 15%.

Crystals were generally soaked or mounted in a stabilizing solution prepared as the crystallization drop, but with the addition of the initial reservoir MeOH percentage and the omission of C-subunit and PKI(5-24). It was discovered that  $Cd^{2+}$  could be substituted for  
30  $Mg^{+2}$  in crystal growth, as with the porcine heart ternary complex crystal. It was also discovered that elevating the  $MgCl_2$  to ten times the starting mother liquor concentration, after crystal growth had stopped, altered the cell dimensions slightly (<1%) and resulted in a different pattern of heavy-atom binding.

### Example 3

Recombinant Binary-Complex Structure Solution

The binary complex crystal was nearly isomorphous with the ternary complex crystal, differing by less than 1% along any axis and had the same space group with  $a = 73.62 \text{ \AA}$ ,  $b = 76.53 \text{ \AA}$ ,  $c = 80.14 \text{ \AA}$ . The asymmetric unit contains one C:PKI(5-24) complex and has a calculated solvent content of 0.53. Mercury reagents were co-crystallized with the C:PKI(5-24) complex by exposing it to 1-mM reagent for six hours, followed by dialysis to remove excess Hg reagent. Native and co-crystallized 4-(hydroxymercuri)benzoic acid (PHMB) derivative diffraction data were measured on the Mark III diffractometer. Data from two native crystals were merged to provide a more complete data set for the initial phase computation, phase extension work, and initial refinement cycles, but later refinement used data from only a single crystal that yielded better quality data. Data from two PHMB co-crystals, one with measured Bijvoet mates, were kept separate and used to compute initial phases, which were improved at constant 3.5- $\text{\AA}$  resolution using the solvent flattening approach of Wang (Methods Enzymol. 115:90, 1985), with a slightly conservative solvent content of 0.50. Additional phases from inversion of the solvent-flattened map were added incrementally using 6 additional envelopes to a final resolution of 2.7  $\text{\AA}$ . Starting with minimap  $\alpha$ -carbon coordinates, the program TOM/FRODO (available from Christian Cambillau, University of Marseille, Marseilles, France) was used with the resulting map to model in the sequence of PKI(5-24) and 257 of the 350 residues in the C-subunit. This partial model was refined using X-PLOR (available from Axel T. Brunger, Yale University, New Haven CT), and calculated structure factors were combined with Wang structure factors in a resolution-dependent manner using equally weighted ABCD coefficients to yield improved maps. ABCD coefficients are described by Hendrickson et al. (Acta Cryst. B26: 136, 1970). Structure solution statistics are summarized in 2, and a sample of electron density of the structure determination is shown in Figure 3, described in detail below.

A number of crystal forms of the catalytic subunit of cAPK have been obtained thus far. All of the crystal forms of the different complexes of the catalytic subunit, with the exception of the monoclinic crystal of the apoenzyme, were obtained under identical crystallization conditions and these are described above. The crystals in different space groups therefore very likely result from conformational states of the enzyme. Crystals of both the binary and ternary complexes with PKI(5-24) exhibited better diffraction characteristics than crystals of the apoenzyme.

Our results also indicate that the ternary complex of the murine catalytic subunit expressed in *E. coli* produced a crystal of better quality than did the ternary complex of the

5 catalytic subunit purified from porcine heart. It is difficult to conclude whether this was due to the absence of myristic acid, the amino acid differences between the two forms, microheterogeneity in the mammalian enzyme, or a combination of these factors. It may suggest, however, that another way to improve the quality of crystals is to mutate the protein and to cocrystallize mutants if crystallization of the wild type fails.

10 Three factors are important for reproducible crystallization. First, the salt of the eluting buffer of the last column must be chosen carefully. Second, the purity of the protein must be verified with isoelectric focusing gels. The protein must not contain typical additives, such as glycerol and should not be frozen prior to crystallization. Third, all reagents used for crystallization must be of the highest degree of purity. If all of these conditions are met, it is possible to obtain, in identical crystallizations, three different crystal forms representing two different conformational states of the enzyme. Some of those crystals, such as those of the ternary complex with PKI(5-24), are of much better quality than the other crystals.

15 The current model consists of C-subunit residues 15-350 and 1-20 of PKI(5-24) and has been partially refined using X-PLOR to an R-factor of 0.195 with r.m.s.(root mean square) bond length deviation from ideality of 0.024 Å. The location of the MgATP-binding site was determined by difference Fourier synthesis with the nearly isomorphous ternary complex crystal, which showed clear density for the adenine, ribose, and  $\alpha$ -PO<sub>4</sub> for the low-[Mg<sup>2+</sup>] ternary complex crystal. The high-[Mg<sup>2+</sup>] difference density showed additional features that could contain the  $\beta$ - and  $\gamma$ -PO<sub>4</sub> as well as metal ion(s), but an unambiguous assignment of atoms to this density could not be made.

20 Diffraction data is summarized in Table 1. Definitions for Table 1 are as follows:  $f_h$ , calculated heavy-atom structure factor amplitude;  $F_p$ , measured native structure factor amplitude;  $F_{ph}$ , measured derivative structure factor amplitude;  $\Delta F_{anom}$ , calculated Bijvoet difference;  $E_{iso}$ , r.m.s. isomorphous lack-of-closure,  $E_{anom}$ , r.m.s. anomalous lack-of-closure;  $R_c = \sum |F_{ph} \pm F_p| - f_h / \sum |F_{ph} - F_p|$ .

30 All diffraction data were measured at 4°C using graphite-monochromated CuK<sub>α</sub> X-rays from the Mark III Rigaku RU-200 rotating anode diffractometer equipped with two Xuong-Hamlin multiwire area detectors. Paired runs starting from settings ( $\omega, \phi, \chi$ ) and ( $\omega, \phi + 180, -\chi$ ) were used to collect Bijvoet mates (inverse beam method). Data reduction and derivative-to-native scaling were done using the UCSD area detector data processing programs (available from San Diego Multiwire Systems).  $R_{sym} = \sum |I_{obs} - I_{avg}| / \sum I_{avg}$  and is shown for merged Friedel pairs.

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Native-1 was used for native. Hg positions of the PHMB (4-(hydroxymercuri)benzoic acid) co-crystal derivative were found from a difference Patterson synthesis. The heavy-atom sites in relation to the model suggest heavy-atom binding at Cys 343 (major site) and Met 58 (minor site). Positional and relative occupancy refinement of two common sites (relative occupancies 2.66, 1.87 for PHMB-1), and calculation of native phases and corresponding ABCD coefficients, were done using the program HEAVY (available from the Protein Data Bank, Brookhaven National Laboratory, Upton, NY). Solvent flattening used the Wang program package (Bi-Cheng Wang, University of Pittsburgh, Pittsburgh, PA) on imported initial ABCD coefficients and phases to 3.5 Å. Molecular envelopes were calculated with solvent content 0.50 rather than 0.53 calculated for the cell. After 3 envelopes at 3.5 Å, the resolution was extended incrementally in 6 shells to a final resolution of 2.7 Å. After convergence at 3.5 Å, the mean phase change/reflection was 36.6° and the mean figure of merit was 0.84; the map inversion R-factor was 0.181. Phase extension added 6786 phases from 5914 in the 3.5-Å starting set; 261 unobserved reflections were estimated by map inversion in the 2.7-Å set.

X-PLOR Version 2.1 was used exclusively following recommended protocols provided in the accompanying manual. Simulated annealing was performed according to a slow-cooling protocol (Brunger et al. Science 235:458-460, 1987) between either 3000K or 4000K and 300K, followed by 120 cycles of conjugate-gradient minimization. Refinement began with the partial model of Stage A to improve the coordinates for phase combination. Combined maps were calculated using the Hendrickson-Lattman scheme. Wang phases were used to 6 Å combined ones between 6 Å and 3.5 Å or 3.0 Å, and calculated phases between 3.5 or 3.0 Å and 2.7 Å. The corresponding weighted amplitudes were  $m_{\text{Wang}}F_o$ ,  $m_{\text{comb}}(2F_o - F_c)$ , and  $m_{\text{sim}}(2F_o - F_c)$ . The model was completed by iterative refinement and building in areas not included in refinement of partial model. Refinement and R-factor ( $= \sum |F_o - F_c| / \sum F_o$ ) calculations used  $F/\sigma > 2$  reflections (12024 Native-1 reflections; 10194 Native-2 reflections beginning with Stage B). The current R-factor of 0.195 is for 2939 atoms (no solvent atoms) with individual B-factors (r.m.s.  $B = 17.6 \text{ Å}^2$ ). R.M.S. bond length and angle deviation from ideality are 0.024 Å and 4.3°.

In summary, the crystals were grown as described above using a 5-10% molar excess of PKI(5-24) and were determined to be of space group  $P2_12_12_1$  with  $a = 73.62 \text{ Å}$ ,  $b = 76.52 \text{ Å}$ ,  $c = 80.14 \text{ Å}$ . The asymmetric unit contained one C:PKI(5-24) complex and had a calculated solvent content of 0.53. Native and co-crystallized 4-(hydroxymercuri)benzoic acid (PHMB) derivative diffraction data were measured using Xuong-Hamlin area detectors.



Data from two native crystals were merged to provide a more complete data set for the initial phase computation, phase extension work, and initial refinement cycles, but later refinement used data from only a single crystal of better quality. Data from two PHMB co-crystals, one with measured Bijvoet mates, were kept separate and used to compute initial phases, which were improved at constant 3.5-Å resolution using the solvent flattening approach of Wang with a slightly conservative solvent content of 0.50. Additional phases from inversion of the solvent-flattened map were added incrementally using 6 additional envelopes to a final resolution of 2.7 Å. Starting with a minima alpha-carbon coordinates, the program TOM/FRODO was used with the resulting map to model in the sequence of PKI(5-24) and 257 of the 350 residues in the C-subunit. This partial model was refined using X-PLOR, and calculated structure factors were combined with Wang structure factors in a resolution-dependent manner, using equally weighted ABCD coefficients to yield improved maps. Details on the combination can be found in Allured et al. Proc. Natl. Acad. Sci. USA 83:1320, 1986 and Remington et al. J. Mol. Biol. 158:111, 1982. An example of the electron density of the structure determination is shown in Figure 3.

Figure 3 is a stereo view of the electron density for the structure determination. Portions of the latest refined model of 3 β-strands are shown (top to bottom from left): 112-106, 114-121, 75-69. Figure 3A provides the 1.5-σ experimental density calculated to 2.7Å using phases after Wang improvement and extensions. Figure 3B provides the 1.5-σ(2F<sub>o</sub>-F<sub>c</sub>) density calculated with 10 to 2.7-Å refined model phases. The current model consists of C-subunit residues 15-350 and 1-20 of PKI(5-24) and has been partially refined using X-PLOR to an R-factor of 0.195 with r.m.s. bond length deviation from ideality of 0.024Å. The structure of the catalytic subunit and effector molecule are described below.

#### Example 4

##### Structural Analysis of the Catalytic Subunit

A stereo view of the backbone structure of the C-subunit with the bound peptide is shown in Figure 4. Residues 15-350 of the C-subunit and the twenty residues of PKI(5-24), in bold print, of the partially refined model are shown. The overall dimensions of the monomer (65Å x 45Å x 45Å) indicate a slightly elongated molecule. Earlier hydrodynamic measurements showing a Stokes radius of 26.1Å, a frictional coefficient ration (f/f<sub>0</sub>) of 1.19, and a radius of gyration of 20Å are consistent with this structure. The most striking feature of the overall molecular architecture is its bilobal shape with a deep cleft between the two lobes. The core of the small lobe is associated primarily with the amino-terminus, while the core of the large lobe corresponds to the C-terminal region of the protein. The cleft

between the lobes is filled by a portion of the bound inhibitor peptide in the binary complex. A difference Fourier map of the ternary complex containing both peptide and MgATP places MgATP at the base of that cleft (Figure 5). The 3.5- $\sigma$  positive density contours for the ( $F_{\text{ternary}} - F_{\text{binary}}$ ) difference Fourier were calculated using refined model phases in 10 to 2.7-Å range and are shown superimposed on the partially refined backbone model. Figure 5A illustrates the general localization of MgATP while Figure 5B is a close-up of difference density enclosing an oriented model of AMP.

The cleft is clearly the site of catalysis, and the peptide-induced conformational changes, observed by both SANS and circular dichroism, may be associated with a closing of this cleft. SANS established that in the absence of inhibitor and MgATP the enzyme adopted a more expanded conformation than that adopted by the enzyme in the binary complex of the enzyme and the peptide inhibitor, or the ternary complex of the enzyme, inhibitor and MgATP. This technique was also used to show that binding of the inhibitor to the enzyme did not require MgATP. Neutron scattering, in particular, established that the apo form of the enzyme adopts a more expanded conformation than the ternary complex containing MgATP and PKI(5-24). Furthermore, PKI(5-24) alone, but not MgATP, was sufficient to induce this conformational change. SANS and CD are techniques known to those of ordinary skill in this art. Accordingly, no further descriptions of these techniques are necessary.

Most of the predictions of secondary structure made prior to this crystallographic study of the C-subunit are quite inaccurate and do not correlate well with the actual structure that is provided herein. The prediction of the secondary structure by Benner et al., Adv. Enzyme Regulat. 31:121, 1991, is somewhat more accurate. It is based on chemical information and homologies within the protein kinase family and is accurate within the small lobe. However, detailed and accurate information on the structures of the protein kinase family has not been available until the discoveries presented herein.

The amino-terminus of the C-subunit begins with an amphipathic  $\alpha$ -helix that lies primarily along the surface of the larger lobe. This N-terminal region differs in the recombinant and mammalian enzymes, since the recombinant protein lacks a myristoyl group at the N-terminal glycine. In the crystal structure, the first 14 amino acids are not visible. However, the surface of the enzyme in this N-terminal region is hydrophobic, suggesting a possible site for the N-terminal myristoyl moiety of the mammalian enzyme. The myristoyl group stabilizes the C-subunit but does not promote association with membranes.

The smaller lobe, consisting of residues 40 through 125, is associated primarily with the binding of the nucleotide and is characterized by a dominance of  $\beta$  structure. Five antiparallel  $\beta$ -strands comprise the core of this domain. The only helical element in the small lobe is inserted between  $\beta$ -strands 3 and 4 and lies on one side of the plane of the  $\beta$ -sheet. It consists of two parts: a two turn helix B, followed by a sharp break and a five turn helix, helix C. Based on a difference Fourier map (Fig. 5) with a ternary complex of the recombinant C-subunit containing MgATP and PKI(5-24), and supported by chemical evidence discussed below, it is clear that this small lobe is the primary site for interaction with MgATP. As seen in Figure 5, the density based on the difference map is consistent with the adenine moiety of the nucleotide oriented towards the base of the cleft beneath the  $\beta$ -sheet, with the phosphates facing outwards, towards the edge of the cleft. This structure is distinct from the Rossmann fold that is characteristic of many nucleotide binding proteins.

The larger lobe, in contrast, is remarkable for its predominance of helical structure. Seven helices are found in this C-terminal domain. A particularly unusual feature are the antiparallel hydrophobic helices, helix E (residues 140 through 159) and especially helix F (residues 218 through 233), that extend right through the core of this domain. The only region of  $\beta$ -structure in this lobe is located on the surface of the cleft at the interface between the two lobes where four antiparallel  $\beta$ -strands form a sheet. Most of the regions important for peptide recognition, as well as some conserved residues likely to be involved in catalysis, are located within this larger lobe.

The C-terminal 70 amino acids, residues 281 through 350, extend over a large portion of the surface of the enzyme from the bottom of the large lobe to the top of the small lobe. The part of this extended chain that passes through the region linking the two lobes appears to participate in recognition of both the peptide and the nucleotide, even though these amino acids are outside the conserved catalytic core. The other extended chain connecting the two lobes of the enzyme, residues 120 through 127, likewise, passes through this linker region between the small and large lobe and also participates in peptide recognition. Hence, this linking region consisting of both chains may contribute in part to the observed peptide-induced conformational changes described earlier. An overall two dimensional topology diagram for the C-subunit of cAPK is presented in Figure 6. Residues corresponding to the secondary structure elements are as follows:  $\beta$ -strands - 1:43-48, 2:57-63, 3:67-75, 4:106-111, 5:115-120, 6:161-164, 7:171-175, 8:178-183, 9:188-191;  $\alpha$ -helices - A:15-31, B:76-82, C:84-97, D:-128-135, E:140-159, F:218-233, G:244-252, H:263-272, I:288-293, J:301-307.

### CORRELATION OF STRUCTURAL DATA WITH CHEMICAL DATA

As discussed above, chemical data can be used to confirm the correct interpretation of the electron density map. Chemical analysis has been used as a way to obtain structural data in the absence of X-ray crystallography. Since the protein kinase family is an enzymatic group of major import, a significant body of chemical data is available. While this data cannot be used to predict a three-dimensional structure for affector modelling, it does provide a body of data that can be used to confirm and ensure the consistency of the three-dimensional structure. Thus, once a crystal structure is obtained for a model enzyme and its affector, the chemical data present in the literature can be used to examine the consistency of the model before proceeding to the design step. The three dimensional structure of the enzyme-acceptor complex should provide a solid explanation for the earlier chemical data. Information provided from chemical data together with structural data is used to obtain the both the template and the "lock" derived therefrom.

For example, evidence for localizing the nucleotide binding site near the amino-terminus first came from affinity labeling with an analogue of MgATP, fluorosulfonyl benzoyl adenosine (FSBA). Labeling with a hydrophobic carbodiimide, DCCD, identified two carboxyl groups near the MgATP binding site, Asp184 and Glu91, and, furthermore, established that Asp184 could be readily cross-linked to Lys72 in the apoenzyme. The structure of the binary complex without bound MgATP (Fig. 7) confirms that all three residues are localized in close proximity to one another, while the difference Fourier map with the ternary complex places these residues close to the  $\gamma$ -phosphate region of MgATP (see Fig. 5). Figure 7 provides stereo views of selected conserved areas.  $1.5\text{-}\sigma$  ( $2F_o - F_c$ ) electron density (10 to  $2.7\text{\AA}$ ) is shown superimposed on the latest refined coordinates. In Figure 7A the sidechains of the invariant Lys72, Glu91, and Asp184 are shown in proximity to each other. Figure 7B shows the catalytic loop, Arg-Asp-Leu-Lys-Pro-Glu-Asn (165-171), together with part of PKI(5-24). Arg 20 of PKI(5-24) is labeled as 365. Lys72 is on  $\beta$ -strand 3, and Glu91 lies along the edge of the C-helix that faces the cleft. Asp184 is located on the loop connecting  $\beta$ -strands 8 and 9, and this loop also lines the cleft. All three residues are invariant in every protein kinase. Therefore these residues can be used as anchors for modeling the three dimensional structure of other protein kinases.

The MgATP binding site was defined more globally by differential labeling with acetic anhydride. By describing the reactivity of each lysine side-chain in the presence and absence of substrates, it was shown by Buechler et al., Biochemistry 28:3018-3024 (1989), that the specific protection afforded by MgATP was localized exclusively to residues in the

small lobe. In addition, to Lys72, MgATP protected Lys76 and Lys47 against modification by acetic anhydride. These protected lysines also flank the conserved glycine-rich loop that lies between  $\beta$ -strands 1 and 2. Based on the difference Fourier shown in Figure 5, this loop is close to the phosphates of MgATP.

5           Chemical studies using an affinity analogue have shown that Cys 199 is important for peptide binding. Modification of Cys 199 leads to loss of activity, and MgATP protects against inactivation. In contrast, Cys 343 can be covalently modified with no concomitant loss of activity. The structural analysis reported here indicates that Cys199 is on the surface of the cleft that interacts with the C-terminus of the inhibitor peptide, and Cys343 is on the  
10           surface of the small lobe. This distance measured between the two  $\alpha$ -carbons of Cys199 and Cys343 in the crystal structure is 24Å. Thus, some of the chemical data is confirmed by the crystal structure.

#### CONSERVED REGIONS AND THEIR FUNCTIONS

15           The fact that all known protein kinases share a conserved catalytic core that is homologous to the C-subunit provides information that independently highlights important regions. This conserved catalytic core begins with the  $\beta$ -1 strand in the small lobe and extends through Arg280 in the large lobe (Hanks et al., *supra*) The two lobes comprising this conserved catalytic core can be seen clearly in Figure 8. Figure 8A is a space-filling model of the catalytic core (residues 40-280) shared by all protein kinases. The small lobe  
20           corresponding to the nucleotide binding fold 1 (residues (40-126); the larger lobe 2 (residues 127-280). In this model the bound peptide is not shown. Figure 8B is a diagram of the conserved catalytic core using the RIBBON program of the PAP package (J. P. Priestle, J. Appl. Cryst. 21:572, 1988 and available from the Molecular Simulation Laboratory at the University of Minnesota, Minneapolis, MN). Regions of the linear sequence noted by  
25           Hanks et al., *supra*, are indicated. The protein kinase having the largest insert at each position is designated using the following notation to define each insert: Gene/Protein Name: NH<sub>2</sub>-terminal C-subunit residue no. (insert length) COOH-terminal C-subunit residue no. The inserts are CDC7:64(14)65, KIN1:83(26)84, PKC- $\gamma$ :98(6)99, c-mos:113(5)114, PDGFR:137(99)138, CDC7:196(82)197, ran<sup>+</sup>:210(23)211,  
30           HSVK:240(11)241, CDC7:260(93)261, 7less:178(7)179. Figure 8C is identical to Figure 8A, but includes PKI(5-24) 3. Within this conserved core are nine invariant amino acids, as well as several highly conserved residues. Most of these conserved residues contribute directly to either MgATP binding or catalysis. Others, such as Arg280 and Asp208, exist as ion-pairs



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and link two segments of the polypeptide chain that are widely separated in the linear sequence.

5 In addition, to providing information on conserved residues, sequence comparisons among protein kinases also identify inserts, sometimes quite sizable, that lie within the catalytic core. These inserts were noted by Hanks et al., *supra*, but their conformation in the overall structure of the catalytic subunit and their relationship to other regions of the catalytic core is described for the first time here. The locations of these inserts are indicated in Figure 8. All inserts invariably are located at loops on the surface of the protein and can be accommodated within the tertiary structure.

10 The structures of several important regions of the catalytic subunit are described below. Two highly conserved loops, as well as a triad of invariant charged residues, appear to be particularly important for nucleotide binding and catalysis. However the regions important for recognition of the peptide substrate are quite variable and were not available until the crystallized structure was analyzed. Predictions based on these variabilities are heretofore undescribed.

#### GLYCINE-RICH LOOP

20 The glycine-rich segment, Gly<sup>50</sup>-Thr-Gly<sup>52</sup>-Ser-Phe-Gly<sup>55</sup>, was identified originally as part of the MgATP binding site based on its proximity to Lys72 and on differential labeling with acetic anhydride, since all of the lysines flanking this region, Lys47, Lys72, and Lys76, are protected in the presence of MgATP. The specific structural explanation obtained from crystallographic data for the protection of Lys47 is due to ionic pairing with the side chain of Glu333 while Lys76 ion-pairs with Glu346. Thus, conformation changes that occur around the glycine-rich loop as a consequence of MgATP and peptide binding are understood from the structural data in combination with known chemical data.

25 A glycine-rich motif is associated with many nucleotide binding sites, and this region has been the subject of much speculation and model building. The Rossmann fold, found in many nucleotide binding sites, contains a sheet of mostly parallel  $\beta$ -strands containing a glycine-rich loop. A similar motif containing a glycine-rich loop is found in other proteins such as adenylate kinase and p21 ras. The protein kinase fold found in the C-subunit and conserved in over one hundred protein kinases, does not conform to either of these motifs; it forms a unique nucleotide binding site. The uniqueness of this site is summarized as follows: (1) The glycine-rich segment lies at a sharp turn that joins two antiparallel strands at the beginning of the  $\beta$ -sheet. (2) The phosphate binding site is not dominated by a helix whose dipole points towards the phosphate. (3) The nucleotide does not lie along the edge

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of the  $\beta$ -sheet. (4) An invariant Lys does not immediately follow this loop. Instead, the invariant Lys in the protein kinases, Lys72, is located in the  $\beta$ -3 strand and is a part of the stable scaffold of the structure. The single conserved element in each of these motifs is the glycine-rich loop whose apparent function is to serve as a phosphate anchor so that the  $\gamma$ - $\text{PO}_4$  is poised for transfer.

#### CATALYTIC LOOP

Another highly conserved loop in the C-subunit extends from Arg165 through Asn171 and can be termed the catalytic loop (Fig. 7B). This catalytic loop, Arg-Asp-Leu-Lys-Pro-Glu-Asn, contains 2 invariant residues, Asp166 and Asn171, and 2 highly conserved residues, Arg165 and Leu167. While the purpose of the glycine loop is to anchor the phosphate moiety and, in particular, to help position the  $\gamma$ - $\text{PO}_4$  so that it is poised for transfer, it is the catalytic loop that appears to be the central hub that communicates to many different parts of the molecule. This loop not only directs the catalytic event, but also guides the peptide into its proper orientation so that catalysis can occur. The loop itself and, in particular, the residues that are important for catalysis are highly conserved, while the parts of the loop that direct the peptide binding are not.

Asp166 is one of 4 invariant carboxyl groups in the protein kinase family. It is the only one that is oriented towards the Ala side chain at the pseudo-phosphorylation site in the bound inhibitor peptide. Asp166 most likely functions as a catalytic base. Catalysis is thought to occur as a direct in-line transfer without an enzyme bound phospho-intermediate.

#### INTERDOMAIN CONTACTS:

The triad composed of the side chains of Lys72, Asp184, and Glu91, shown in Figure 7A, is conserved in every protein kinase and is close to the  $\gamma$ - $\text{PO}_4$  of MgATP. Asp184 was a candidate for the catalytic base; however, the structure indicates that a more plausible role is participation in the chelation of  $\text{Mg}^{2+}$  in the MgATP complex. The side chain of Asp184 also comes within 4-5Å of the side chain of Asn171. This cluster, Asp184, Asn171, and Asp166, thus forms a second triad of invariant amino acids. Asp184, being a component of both triads, has the potential to shuttle between the two conserved loops, the glycine-rich loop in the small lobe and the catalytic loop in the larger lobe. Hence, if the position of Asp184 changes following the binding of MgATP, as it probably will given its location in the structure relative to the MgATP binding site, the consequences will have a direct impact on both conserved loops. If, for example, Asp184 participates in the chelation of  $\text{Mg}^{+2}$ , its negative charge would be sequestered from the catalytic loop, thus allowing the other

residues to rearrange in order to maximize the nucleophilicity of the serine hydroxyl moiety that is poised to receive the phosphate from ATP.

This is the first protein kinase structure to be reported. The protein kinases represent a large family of over 100 enzymes that includes growth factor receptors as well as many oncoproteins. In spite of the tremendous diversity of these enzymes, all share a conserved catalytic core that retains the same essential features of secondary and tertiary structure and the same general mechanism of catalysis. The essential hallmarks of this conserved core include: (1) two lobes with a cleft between that is occupied by the substrates, (2) a unique nucleotide binding fold dominated by  $\beta$ -structure, (3) a largely helical domain associated with peptide binding and catalysis, (4) two  $\beta$ -sheets converging at the active site near the domain interface, and (5) two conserved loops, one in each lobe, that converge at the active site. In marked contrast to these conserved features shared by all protein kinases, recognition of the peptide by the catalytic subunit involves non-conserved amino acids, and the peptide binding sites extend over diverse and widely separated regions on the surface of the enzyme. The detailed structure of the bound inhibitor peptide and its specific interactions with the catalytic subunit are described below.

Affector binding site data may incorporate information derived from several experimental avenues. In addition, to crystallographic studies, substrate analogues provide insights into the specific features of a given substrate that are important for recognition. Chemical approaches such as affinity labeling and group specific labeling can identify regions and specific residues that are in close proximity to substrates. Crystallographic studies can include a structural analysis of the apoenzyme, i.e. the structure of the enzyme without other associated molecules. However, more importantly, crystallographic studies of co-crystals of the enzyme with bound substrates or effectors are provided, so that the precise features of the active site can be defined.

Thus, in the model system of the present invention, crystals of the cAMP-dependent protein kinase C-subunit/PKI(5-24) were obtained and structural data derived therefrom. This structure of the catalytic subunit is presented as example 4. The inhibitor peptide PKI(5-24) is a fragment of the heat stable protein kinase inhibitor. Additional information about this inhibitor can be found in a publication by H.-C. Cheng et al. (Biochem J. 231:655-661, 1986). This peptide includes the consensus features common to all peptide substrates and inhibitors of cAMP-dependent protein kinase. In addition, it contains other features that convey unique high affinity binding. The crystals of complexed enzyme and inhibitor

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provide insight into the guidelines necessary for designing effector molecules for other protein kinases.

5 The general requirements for peptide recognition by the catalytic subunit were characterized originally using synthetic peptides. These studies found a consensus sequence that includes two basic residues, typically arginines, followed by one intervening small residue preceding the site of phosphotransfer. The phosphate acceptor site, either Ser or Thr, is followed immediately by a large hydrophobic residue. The typical peptide substrate used for this kinase, based on the phosphorylation site in pyruvate kinase, is shown in Table 2. Replacement of the Ser with an Ala generates an inhibitor peptide with poor affinity. 10 In contrast is the inhibitor peptide, PKI(5-24), derived from the thermostable protein kinase inhibitor (PKI). This peptide, seen in 2, encompasses the consensus sequences described above but also contains additional unique features that convey high affinity binding. The particular features that contribute to high affinity binding were defined using peptide analogues, and the most important ones are also indicated in 2. This peptide, PKI(5-24), 15 was co-crystallized with the catalytic subunit, and the structure of that peptide as well as its interaction with the protein are discussed below.

A schematic of substrate and inhibitor peptides of cAMP-dependent protein kinase are provided in Table 2. The nomenclature used for the peptides designates the phosphorylation site or pseudophosphorylation site residue as P. In the case of substrates, 20 P will be Ser or Thr; in the case of PKI(5-24), P is Ala. The residues flanking this site are designated as P+1, P-1, etc. as indicated. This nomenclature provides a common frame of reference for all peptide substrates and inhibitors and can be invoked readily for every protein kinase.

The Ser peptide is based on the *in vivo* phosphorylation site in pyruvate kinase. 25 Residues shown to be important for peptide recognition are shaded and were identified using synthetic peptide analogues of the Ser peptide and of PKI. Procedures for determining which residues are important for peptide recognition using peptide analogues can be found in articles by Glass et al. and Kemp et al. (J. Biol. Chem. 262:8802-8810, 1989 and J. Biol. Chem. 252:4888-4894, 1977 respectively.)

30

#### Example 5

##### Conformation Determination of the Bound Inhibitor

The conformation of bound PKI(5-24) is shown in Figure 9. Backbone C and N atoms are shown in bold. Residues particularly important for binding are labelled according to the nomenclature of 2. The amino-terminus extending from the P-16 Thr through the P-8

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Ala forms an amphipathic  $\alpha$ -helix. This helix is followed by a turn flanked by glycines at the P-7 and P-4 positions. The glycines may be important for accommodating the turn or for providing flexibility to facilitate binding of the Arg that follows each Gly. The remainder of the peptide is in an extended conformation, and the density corresponding to the region at the C-terminus, the P+2 Asp and the P+3 His, is not well defined.

The catalytic subunit itself consists of 2 lobes - a smaller lobe, associated primarily with MgATP binding, and a larger lobe. Nearly all of the features necessary for peptide recognition are found within the larger lobe, although the specific residues involved are widely dispersed both in the linear sequence and on the surface of the enzyme. The extended portion of the peptide that includes the consensus region for recognition of all substrates and inhibitors lies along the surface of the cleft corresponding to the larger lobe. The helical segment of the peptide is amphipathic, and its hydrophobic side lies in a hydrophobic pocket on the surface of the large lobe. The specific interactions of the peptide with the protein can be described by (i) the interactions that account for the unique highly affinity binding of PKI and (ii) by the features of the protein that are important for recognizing the consensus sequence common to both the inhibitors and substrate.

#### HIGH AFFINITY BINDING SITE

Based on the crystal structure, the high affinity binding attributed to the N-terminus of PKI(5-24) is dominated by hydrophobic interactions involving primarily the phenylalanine side chain at the P-11 position. Glass et al. showed that a replacement of this Phe with an Ala caused a 100-fold increase in  $K_i$  while replacement with 1'-naphthylalanine, a residue that is considerably larger and more hydrophobic than Phe, actually decreased the  $K_i$  by 4-fold. Figure 10 illustrates the high affinity binding site interactions. A hydrophobic pocket on the surface of the C-subunit nicely complements the hydrophobic face of the helix in the inhibitor peptide. This hydrophobic pocket is lined by residues 235 through 239, Tyr-Pro-Pro-Phe-Phe, with the phenyl ring in the inhibitor peptide sandwiched between the side chains of Tyr235 and Phe239. In Figure 10A the P-11 Phe ring (numbered 356) is shown in relation to three nearby hydrophobic residues of the C-subunit: Tyr 235, Pro 236, and Phe 239. Figure 10B illustrates the interactions of the P-11 Phe and P-6 Arg sidechains with the C-subunit. Distances between charged-residue sidechain atoms  $<3.5\text{\AA}$  apart are indicated by thin connecting lines. Based on the structure, the Tyr at the P-14 position is not essential for this hydrophobic interaction. In addition, to the hydrophobic interactions associated with the helix, the orientation of the high affinity binding region PKI(5-24) is fixed by the ionic



contacts involving the P-6 Arg. Two nitrogens in the guanidine side chain of this Arg undergo ion-pairing with the two oxygens of the carboxyl group of Glu203.

### CONSENSUS RECOGNITION SITE

Figure 11 summarizes the interactions that contribute to recognition of the common consensus region of the inhibitor peptide. The interactions of the P-3 and P-2 Arg residues and the P+1 Ile residue with C-subunit residues are shown. Lines are drawn between charged-residue sidechain atoms <3.5Å apart. The P+1 Ile sidechain projects into the hydrophobic area formed by Leu 198, Pro 202, and Leu 205. Electrostatic interactions dominate the portion of the peptide proximal to the site of phosphotransfer, while hydrophobic interactions dominate the C-terminal region distal to the phosphotransfer site.

Two important requirements for peptide recognition by cAPK are basic residues at the P-3 and P-2 positions. Others have shown that replacing either Arg in the Ser peptide substrate leads to a 16-400-fold increase in  $K_m$ , even when the Arg is replaced with a Lys. The environment flanking the P-3 and P-2 arginines explains these results since each Arg interacts with more than one carboxyl side chain.

Table 3 provides a listing of the amino acid residues present at the various points of contact between PKI(5-24) and two protein kinases, cAPK and casein kinase II (CKII). It can be seen from Figure 11 and Table 3 that in the C subunit of cAPK, that those residues lining the p+1 site are very hydrophobic and provide a pocket for the hydrophobic p+1 residues. In CKII, the residues lining this pocket are all basic or positively charged. This basic pocket compliments an acidic residue at the p+1 position and this is consistent with the known specificity of CKII, i.e. CKII prefers acidic groups at the p+1 position.

Figure 12 provides information on the consensus recognition site binding interactions. The electron density corresponding to the anionic P-3 site is shown in Figure 12A. Residue numbers 361, 364, 365, and 368 correspond respectively to PKI(5-24) P-6, P-3, P-2, and P+1 residues. The electron density of the P-3 Arg sidechain tip is shown in proximity to Thr 51 carbonyl in the glycine-rich loop, and Glu 127 and Glu 331 sidechain carboxylates of the domain-linking region. In Figure 12B the  $1-\sigma$  ( $2F_o - F_c$ ) electron density of the P-2 Arg sidechain is shown in proximity to sidechain carboxylates of Glu 170 of the catalytic loop and Glu 230; the P-6 Arg sidechain is shown near sidechain carboxylate of Glu 203. In Figure 12C the  $1.5-\sigma$  ( $2F_o - F_c$ ) electron density of the P+1 Ile sidechain is shown projecting into a hydrophobic pocket comprised of residues Leu198, Pro202, and Leu205. The side chain of this P-3 Arg interacts with Glu127. The carboxyl side chain of Glu331 also is approximately 3Å from the guanidinium nitrogens. The tip of Asp329 is approximately

5Å away. Thus, the position of the guanidinium moiety is fixed. In addition, the side chain of the P-3 Arg comes close to the backbone carbonyl of Thr51 in the glycine-rich loop and to the hydroxyls of the ribose ring. The side chain of Glu333 lies close to Lys47 in  $\beta$ -strand 1, and the side chain Glu334 is approximately 3Å from the hydroxyl group of Thr48.

5           The P-2 site is also very anionic, and this Arg, likewise, interacts with more than one carboxyl group. As indicated in Figures 11 and 12B, the  $\epsilon$ -nitrogen forms an ion-pair with Glu170, while one of the terminal nitrogens interacts with Glu230. Glu 203 also comes close to this guanidinium side chain; however, its interaction with the P-6 Arg is dominant. In the absence of an Arg at the P-6 position, Glu230 may ion-pair with the P-2 Arg. Unlike the  
10   P-3 recognition site, all of the carboxyl groups at the P-2 site are an integral part of the large lobe.

#### DISTAL HYDROPHOBIC SITE (P+1)

          Peptide analogue studies of others predicted a hydrophobic requirement at the P+1 position since replacement of the Leu with Gly in PKI(5-24) caused a 150-fold increase in  
15    $K_m$ . The reasons for this requirement are now clear from the structure (Figs. 11 and 12C). Leu198, Pro202, and Leu205 form a hydrophobic groove that surrounds the Ile side chain. This hydrophobic region that constitutes the P+1 site lies at the edge of the cleft and is likely important for proper orientation of the actual site of phosphotransfer at the P position. In the binary complex this region begins to align in an antiparallel  $\beta$ -like  
20   configuration with the carbonyl of the P+1 Ile coming less than 4Å from the backbone amide of Gly200 and the carbonyl of Gly200 coming within approximately 3Å of the backbone amide of this Ile at the P+1 position (Fig. 13B). Substitution of a Pro for Leu at the P+1 position in the Ser peptide (2) yields an extremely poor substrate. Nevertheless, a depsipeptide analogue of this peptide lacking an amide proton at this P+1 site is still a  
25   good substrate for the catalytic subunit.

          Figure 13 illustrates the catalytic site area. Residue numbers 364 and 367 correspond to the P-3 Arg and the P Ala.  $1.5-\sigma$  ( $2F_o - F_c$ ) electron density is shown in all cases. Figure 13A provides the site of catalysis together with the possible catalytic base sidechain of Asp 166 near the  $\beta$ -C of the P Ala. Thr 51 of the glycine-rich loop is shown  
30   near the P-3 Arg sidechain, and hydrophobic sidechains of residues Phe 54 (at the loop apex) and Phe 187 are shown near the site of phosphotransfer. The addition of a hydroxyl group would place the side chain of the residue at the P position close enough for a direct transfer of the  $\gamma$ -phosphate for MgATP. The side chain of the P-1 Asn also interacts with the glycine-rich loop as shown in Fig. 13A. Figure 13B diagrams the consensus recognition

site residues Arg-Arg-Asn-Ala-Ile together with the glycine-rich phosphate anchor loop to the left and residues 198-202 to the right. The term "residue" is here used interchangeably with amino acid. The carbonyl of Gly 200 can be seen pointing to the amide N of the P+1 Ile. Figure 13C shows the phosphate of Thr 197 buried among sidechains of cationic and H-bonding residues (His 87, Arg 165, Lys 189, Thr 195). Cys 199 is also shown nearby.

Thr197, one of the two stable phosphorylation sites in this enzyme, also flanks the P+1 site. Multiple electrostatic interactions, seen in Figure 13C, hold this  $\text{PO}_4$  in place and account for its resistance to removal by phosphatases. Fixing this phosphate moiety contributes conformational stability, not only to Thr197 but also to the adjacent hydrophobic residues important for recognition at the P+1 site and for the proper orientation of the site of phosphotransfer. Based on the crystal structure, this anionic group appears to be important for the final correct assembly of the structure.

#### CORRELATION WITH EXPERIMENTAL PREDICTIONS

Several chemical approaches identified amino acid side chains that contribute to peptide recognition. Differential labeling with a water soluble carbodiimide, 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (EDC), targeted solvent-accessible carboxyl groups that were accessible in the free C-subunit but protected in the presence of substrate (Buechler et al. Biochemistry 29:1937-1943, 1990). Two regions were identified using this approach. Glu170 was very reactive in the absence of peptide, but fully protected in the presence of peptide. The other region was the cluster of carboxyl groups near the C-terminus, Asp<sup>328</sup>-Asp-Tyr-Glu-Glu-Glu-Glu<sup>334</sup>. As indicated in Figure 12, Glu170 interacts with the P-2 Arg while the cluster of carboxyl groups flanks the P-3 site.

The crystal structure localized Cys199 close to the peptide recognition site and to the  $\gamma\text{-PO}_4$  subsite of ATP. In the binary complex, Cys 199 does not appear to participate in peptide binding other than to contribute to the general hydrophobic environment around the P+1 site.

#### CONFORMATIONAL CHANGES ASSOCIATED WITH PEPTIDE BINDING

Substrate-induced conformational changes are associated with peptide binding to the catalytic subunit. Global changes in conformation, first observed using circular dichroism, showed both a loss of alpha-helical content and an increase in beta structure following peptide binding. A global change in shape also was observed using low angle neutron scattering. These results demonstrated a reduction of the radius of gyration ( $R_g$ ) following substrate binding and furthermore established that the inhibitor peptide alone, but not MgATP, was sufficient to cause the reduction in  $R_g$ . The substrate-induced reduction in  $R_g$

indicates that the apoenzyme corresponds to an open configuration of the protein while the binary and ternary complex represent a closed configuration.

5 The recognition of the peptide by the catalytic subunit is believed to be a multistep process. The initial step, associated with a loss in  $\alpha$ -helical structure, was induced by both the substrate and inhibitor heptapeptides shown in 2. The second step, presumably corresponding to the final orientation of the peptide into the correct position at the active site, was associated with an increase in  $\beta$ -structure and could only be accomplished with the substrate peptide, not by the Ala peptide inhibitor. This increase in  $\beta$ -structure is probably due, in part, to the P+1 region of the peptide interacting the protein. Understanding these  
10 substrate-induced conformational changes will eventually require a detailed comparison of the apoenzyme structure with binary and ternary complexes containing inhibitors and substrate peptides both in the presence and absence of MgATP.

The peptide-induced conformational changes in catalytic subunit may reflect a closing of the cleft and probably involve the region linking the small and large lobes as well. This  
15 linker region consists of two chains: residues 123 through 127 and a highly acidic segment, residues 328-334. The P-3 peptide binding site is the only region of the inhibitor peptide that interacts directly with both of these extended chains that link the two lobes. One anionic group at the P-3 site is Glu127 and the other is Glu331. Since several of the carboxy groups in the C-terminal linking chain also interact with portions of the nucleotide binding  
20 site, even in the binary complex, this P-3 residue may contribute to the substrate-induced conformational changes.

#### CONSERVED AND VARIABLE SITES IN PROTEIN KINASES

The recognition of a protein substrate by the catalytic subunit is not unlike the recognition of a protein antigen by the variable domain of an immunoglobulin. The binding  
25 sites of both structures are dominated by interfacing  $\beta$ -sheets surrounded by loops that participate in recognition of the protein. The catalytic subunit also has helical regions, but it is the  $\beta$ -sheets that converge at the active site and it is the loops that play the dominant role in peptide recognition and catalysis. One  $\beta$ -sheet comes from the small lobe and the other from the large lobe. These two sheets are sandwiched together at the cleft. In the  
30 case of protein kinases, two of the loops are essential for catalysis and are highly conserved, unlike the immunoglobulins, whose function is only to bind antigens.

The two essential conserved loops that assemble at the site of catalysis in the catalytic subunit, seen in Figures 14 and 15, are the glycine-rich loop in the small lobe and the catalytic loop in the large lobe. Both lie on the surface that lines the cleft between the

two lobes. The glycine-rich loop serves as an anchor for the phosphates of MgATP, whereas the catalytic loop is essential for peptide binding and catalysis. Key features of the active site of the catalytic subunit are shown in Figure 14. Nine of the amino acids that are nearly invariant in all protein kinases are indicated. Gly186, another invariant residue, is not shown. The alpha carbons are in black, oxygens dotted, and nitrogens in horizontal hatching. The position of the phosphorylation site at Thr197 is indicated by vertical hatching. The portion of the active site associated with the small lobe is shaded and includes three of the invariant amino acids, Gly 52, Lys72, and Glu91. The remaining six are located in the large lobe. Residues close enough for hydrogen bonding or ion pairing are indicated by a dashed line while residues within 4-5 Å of one another are connected by a dotted line. As seen in Figure 14, seven of the nine invariant amino acids conserved in all protein kinases are located here, either in the loops themselves or connecting directly with loop residues. The single invariant glycine, Gly52, lies in the phosphate anchoring loop. The proposed catalytic base, Asp166, as well as Asn171, are in the catalytic loop. It is remarkable how thoroughly interconnected this region is with multiple ion pairs providing a finely tuned scaffolding for communication at the active site.

The three invariant residues in the small lobe all participate in nucleotide binding. Unlike Gly52, which is part of a flexible loop, both Lys72 and Glu91 are anchored to defined parts of the secondary structure - Lys72 to  $\beta$ -strand 3 and Glu91 to the C-helix. The difference Fourier map shows the phosphate density near these residues, with the presumed  $\gamma$ -PO<sub>4</sub> density close enough to the P Ala C <sub>$\beta$</sub>  for phosphotransfer were it a Ser[Thr] and indicates that these residues play a key role in the recognition of the phosphates of MgATP.

In the catalytic loop the two invariant residues, Asp166 and Asn171, interact with each other. Not only are their side chains close, but, more importantly, the nitrogen in the amide side chain of Asn171 is less than 3Å from the backbone carbonyl of Asp166. One additional nearly invariant residue, Asp220, contributes directly to stabilization of the catalytic loop. The two oxygens of this carboxylate come with hydrogen bonding distance of the backbone carbonyl and amide of residue 164 that immediately precedes the loop. The interaction of the catalytic loop with a conserved residue that lies deep within the large lobe fixes the loop from one side while peptide binding and interactions with the small lobe fix it from the opposite direction. As seen in Figure 13A and 13B, the consensus region of the peptide is sandwiched between the P+1 site on one side and the glycine-rich loop on the other side.



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Of all the invariant residues, Asp184 is the only one that appears to communicate with both the small lobe and the large lobe. In the binary complex, it is most closely associated with Lys72, but it is also only 4-5Å from Asn171 and Asp166 in the catalytic loop. Although not shown in Figure 14, Asp184 is itself part of a tight turn with the carboxylate located within hydrogen bonding distance of the backbone amide of Gly186, another invariant residue. This entire segment, Asp166-Phe-Gly, is highly conserved in all protein kinases, and hydrogen bonding to stabilize the turn is probably conserved as well. Asp184 certainly has the potential to shuttle between the two conserved loops, and it is anticipated that the contacts of Asp184 will differ somewhat in both the apoenzyme and in the ternary complex containing bound MgATP as well as peptide. If Asp184 participates in the chelation of  $Mg^{2+}$ , as disclosed above, then this charge will be sequestered from the immediate environment of the catalytic loop. Other residues close to the conserved residues in the catalytic loop in the binary complex are Tyr164 and Lys 168. The Tyr 164 side chain is less than 3Å from the side chain nitrogen of Asn171, and the Lys168 side chain comes close to the carboxylate of Asp166. Either Tyr or His, another good hydrogen-bonding residue, is always found at position 164, so this contact can also be conserved. Any significant change in the position of Asp184 will likely change the environment of the catalytic loop. Asp184, as well as Asn171 and Asp166, have also been identified as a sequence motif associated with many phosphotransferases, and this may represent a common mechanism among protein kinases.

The versatility and importance of the catalytic loop is highlighted not only by the conserved networking of essential amino acids at the active site, but also by the special ways in which this conserved network communicates with the variable residues that compose the peptide binding sites. This communication specifically involves loop residues that are not highly conserved. Glu170, for example, contributes directly to the anionic P-2 site. Thr201 in the P+1 site, on the other hand, comes very close to the side chain of Asp166. These two particular regions of contact involving the peptide binding site and the catalytic loop, Lys<sup>168</sup>-Pro-Glu and Thr<sup>201</sup>-Pro-Glu-Tyr-Leu-Ala-Pro-Glu, contain sequences that differ characteristically between the kinases that transfer phosphate to Ser/Thr and those that transfer phosphate to tyrosine (Hanks et al., supra).

Arg165 is actually highly conserved in most protein kinases, and it connects in a unique way with the P+1 peptide binding site. Specifically, it points towards the phosphothreonine and helps to fix that phosphate so that the hydrophobic groove that follows and provides a pocket for the side chain of the P+1 residue is firmly positioned

(Figure 13C). This is an autophosphorylation site, and it is the only phosphorylation site in the catalytic subunit that could conceivably result from an intramolecular autophosphorylation. Chemical analysis has shown that this phosphate is very resistant to removal by phosphatases and based on this crystallographic data, appears to contribute to the final conformation stability of the enzyme. It should be emphasized as well that a phosphorylation site in this region of the protein is not a conserved feature of all protein kinases. Some kinases such as pp60<sup>C-src</sup>, a protooncogene whose viral counterpart is found in Rous Sarcoma Virus, do have an autophosphorylation site nearby, but many others do not. Whether the catalytic loop communicates in unique ways with other autophosphorylation sites in other protein kinases remains to be established.

The two invariant residues that are most distant from the active site are Asp208 and Arg280. These residues constitute a conserved ion pair that lies just beneath the P+1 site and appears to stabilize a very hydrophobic region that buttresses the P+1 peptide binding site.

Figure 15 is a schematic of the conserved and variable regions of the catalytic subunit. The ribbon diagram depicts the folding of the catalytic subunit. Conserved regions include two loops - the glycine-rich loop and the catalytic loop - and are indicated. The variable peptide binding sites are shown as solid areas. Invariant amino acids Gly52, Lys72, Glu91, Asp166, Asn171, Asp184, Glu208, Asp220, and Arg280 are indicated by a large dot and are numbered. Dashed lines indicate residues that are close enough to pair, while the dotted line extends from Arg165 to the Thr197. Several points should be emphasized regarding the recognition of a peptide or protein substrate by the catalytic subunit. First is the number of sites and their diversity. Some of these peripheral peptide recognition sites are hydrophilic and highly charged; others are hydrophobic. As seen in Figure 15, most are found within the large lobe of the catalytic core shared by all protein kinases, but some also lie outside of this boundary. A second observation is that the requirements for recognition at the consensus site are not absolute. A comparison of *in vivo* phosphorylation sites reveals that the actual residues at each site vary somewhat as does the spacing between the positively charge side chains and the site of phosphotransfer. Thus, even in the consensus region, some variability can be tolerated. A third point is the potential for variability in recognition of different inhibitor, and presumably substrate, proteins that bind with a high affinity to the catalytic subunit. Most of the features essential for the high affinity recognition of PKI are apparent from this structure of the binary complex. The regulatory subunit, however, also binds to the C-subunit with a subnanomolar affinity in the absence

of cAMP. The consensus region, P-3 through P+1, is shared by both molecules. However, the R-subunit, cleaved at the P-5 position, still retains its high affinity binding for the C-subunit. In addition, the P-16 to P+1 region of the R<sup>I</sup>-subunit is Pro-Pro-Pro-Pro-Asn-Pro-Val-Val-Lys-Gly-Arg-Arg-Arg-Arg-Gly-Ala-Ile, and this certainly cannot conform to the helical motif that dominates the corresponding region of PKI(5-24). Hence, an amphipathic helix is not required for the high affinity binding of the regulatory subunit. Instead, the residues that contribute to the high affinity binding of the regulatory subunit, specifically, must lie beyond the P+3 position and may complement a different portion of the surface of the C-subunit. This variability presumably can also extend to protein substrates where the catalytic subunit may recognize unique sequences that lie outside the consensus site.

Unlike the conserved residues that are invariant in all protein kinases, the sites involved in peptide recognition differ for each kinase. About 30% have some general similarities to cAPK. Others are quite different. However the template allows us to predict the specificity of each contact point. Figure 16 provides the sequence of PKI(5-24) and illustrates the distances between the points of contact and the catalytic site in three-dimensional space as measured from the template. The P site or site of catalysis is denoted by an arrow. Asterisks designate sites particularly important for the high affinity binding of PKI(5-24). Recognition sites essential for PKI binding to other substrates are denoted as labelled archways p+1, p-2, p-3, p-6, and p-11. All of the distances, with the exception of the p+1 site, are greater than 5 Å. That positions 5 Å or greater from the site of catalysis are important for inhibitor specificity have heretofore been undisclosed.

The identification of the subsites that are important to maintaining the specificity of the effector molecule interaction and provide K<sub>d</sub> less than 100nM facilitates the design of other inhibitors. PKI(5-24) can be used as a scaffold for molding new inhibitors, and in addition once the electrochemical interactions are understood from an analysis of the three dimensional template, other effectors that are not peptides can additionally be identified. Thus, effectors could come from a group including but not necessarily limited to peptides, polypeptides, unmodified molecules existing in nature, synthetic molecules, nucleic acids, polymers, organics, or hydrocarbons. Molecules that exist in nature and that are known to interact with enzymes could be modified to produce effector molecules. Examples from this group include antibodies, antibiotics, protein, other enzymes, lipids, polysaccharides, saccharides and vitamins. Thus, inhibitors can be designed that utilize both conserved and nonconserved points of contact.

The invariant residues within the protein kinase family and specifically, cAPK, are used to apply the template and its coordinates to other protein kinases. There are 8-9 invariant residues for the protein kinase family. Other families may have differing numbers of invariant residues. Table 4 list the invariant residues and the distances between these  
5 residues. The distances are calculated between  $\alpha$ -carbons. The distances between residues 52, 72 and 91 are expected to remain close to constant since these residues are all in the amino-terminal domain of the protein. Similarly, the distances between residues 166, 171, 184, 186, 208 and 280 would be expected to remain constant due to their being in the carboxy-terminal domain. Motion of the amino-terminal domain relative to the carboxy  
10 terminal domain is expected to change the distances between residues in different domains.

The distances calculated in Table 4 help form the model template since these three-dimensional positions are taken from the crystal diffraction patterns and help to define a conserved shape for the protein kinase family catalytic core. A point of contact is defined herein to occur at the invariant residues and is additionally defined as a point of close  
15 spatial approximation between the atoms of the residues within or around the catalytic core and the atoms of the effector. These points of contact affect the specificity and the Kd of the enzyme/effector interaction.

The template is best described by Figure 11. The coordinates for the template listed in Table 4 and Figure 17 provide the spatial characteristics that permit one of skill in the  
20 art to input the template structure into a computer program and perform the invention disclosed herein. While the coordinates together define a three-dimensional surface that permits visualization of the catalytic site, there are invariant residues that establish important foci within the structure.

Lys 72 is invariable within the catalytic site for the protein kinase family and is an  
25 anchor for superimposing other protein kinases onto the template. Asp 166 can additionally be a second important anchor. Similarly the other invariant positions likewise have importance for fitting other kinases. A combination of the coordinates with the invariant residue positions allows important regions within and around the catalytic site to be visualized. From a study of the interaction of cAPK with PKI(5-24), important hydrophobic  
30 and ionic interactions can be analyzed. When a new enzyme is superimposed onto these coordinates these hydrophobic and ionic interactions are assessed with PKI(5-24). It is then possible to study what changes can be made to PKI(5-24) to model a new effector. A study of the residue sidechains and the charge distribution within the site is used to fine tune the new effector.

Any protein kinase having homology in and around the catalytic site with cAPK can be used to design specific effector molecules. Hanks et al. provides a list with homologous residues highlighted. Many growth factor receptors have protein kinase activities. These include but are not limited to platelet-derived growth factor, colony stimulating factor, the insulin receptor family and epidermal growth factor. Protein kinases are involved in hematopoiesis and lymphopoiesis. Some, like myosin light chain kinase, are calcium-calmodulin dependent, and further, a variety of protein kinases are oncogenic products. These include but are not limited to viral and cellular homologues of src, mos, abl, Neu, Fgr, and Yes. Any of these kinases as well as others fitting the characteristics disclosed herein could be used in this invention to produce specific effector molecules.

The phosphorylation target sequences are available for a variety of protein kinases. These include phosphorylatable amino acids with their surrounding residues. For some kinases this will provide a good starting point for inhibitor design. Other protein kinases have a regulatory subunit associated with the catalytic subunit in the inactive form. The binding sequences with the regulatory subunits are other starting points for effector molecule design. Additionally, there are a group of protein kinases that have a regulatory domain. This domain binds the catalytic site when the enzyme is inactive. Binding of an exogenous molecule changes the kinase conformation such that the regulatory domain no longer binds. A review by Pearson et al. provides a table of protein kinase phosphorylation site sequences (Methods in Enzymology Vol. 200, 1991 in press).

Once a template is created there are several options available for designing an effector molecule and these were outlined in the section above entitled "Brief Description of Effector Design."

#### EXAMPLE 6

##### Inhibitor design for pp60<sup>c-src</sup> without pp60<sup>c-src</sup> purification

pp60<sup>c-src</sup> is the proto-oncogene homologue of the src protein kinase from Rous Sarcoma Virus. The protein causes unrestrained cell proliferation. In this example, the invariant residues for pp60<sup>c-src</sup> are identified with a star and in bold below:

ESLRLEVKLGQGC**FGE**VWMGTWNGTTRVAIKTLKPGTMSPEAF**LQEAQVMKKL**  
RHEK**LV**

OLYAVVSEEP**IYIVTEY**MSKGSLLD**FLKGETG**KYLRLPQ**LV**DMAAQ**IASG**MAYBE  
RMNY



-52-

VHRDLRAANILVGENLVCKVADFGGLARLIEDNEYTARQGAKFPIKWTAPEEAALY  
GRFTI

5 KSDVWSFGILLTELTTKGRVPYPGMVNREVLQVERGYRMPCPPECPESLHDLH  
CQCWR

•  
KEPEERPTFEYLQAFLEDYFTST

10 These residues are incorporated into the appropriate position from the invariant  
residues listed in Table 4 using the coordinate set provided in Figure 17. Once the template  
is in place and the catalytic site from pp60<sup>c-src</sup> has been superimposed onto the template,  
it is possible to visualize the catalytic site. The site can additionally be refined using the  
complementary target phosphorylation site for pp60<sup>c-src</sup>.

RLIEDNEY\*<sup>\*</sup>TARQGAK

15 \* denotes the site of phosphorylation.

Residues are altered using computer modelling until a fit is achieved for pp60<sup>c-src</sup>  
on the template. Thus, residues 184, 166, 172, 220, 208, and 280 from the pp60 c-src  
sequence have positions in space that maintain those distances disclosed in Table 4. Ionic  
and hydrophobic amino acid side chains are matched within the catalytic core with  
20 complementary residues to create a new inhibitor molecule. Recombinant cAPK is then  
mutated to duplicate the three-dimensional structure within the core. Crystals of mutated  
cAPK are analyzed alone or together with a proposed inhibitor. The structure is again  
analyzed in the context of the invariant residues listed in Table 4.

Positions 52, 72, and 91 are mobile invariant residues whose positions will vary  
25 depending on the quality of inhibitor. The distances of these residues are listed in Table  
4 for PKI(5-24) and cAPK. It is anticipated that peptide inhibitors of equal affinity for  
cAPK will have similar distances. Non-peptide inhibitors can be designed that do not  
produce a rotation, or fraction of fit, exactly in the same direction as peptide inhibitors, such  
as PKI(5-24). A comparison of the crystal structure of cAPK and cAPK with PKI(5-24)  
30 indicate that positions 52, 72 and 91 rotate 12° toward residues 184, 166, 172, 220, 208 and  
280. This rotation defines a range of peptide inhibitors. Another strong peptide inhibitor  
will similarly produce a 12° rotation toward the six residues listed above while residues 52,  
72 and 91 may have a smaller angle of rotation for weaker peptide inhibitors.

In addition, there are important points of contact between cAPK and PKI(5-24).  
35 The specific contact amino acids on PKI(5-24) are starred and the corresponding points of  
contact within the catalytic core of cAPK are identified as positions p+1, p-2, p-3, p-6 and  
p-11. These points of contact are conserved within the catalytic core of all protein kinases

and similar points of contact will be readily identifiable to those of skill in the art for other protein kinases. A sphere of influence having a radius of 11Å or less, more preferably 6Å or less, and extending from the inhibitor around the points of contact at positions p+ 1, p-2, p-3, p-6, and p-11 can be used to define regions that are critical for inhibitor specificity.

5           As described above, in connection with Figure 11, the points of contact can be used to identify the replacements necessary to design appropriate inhibitors or other effectors for a new enzyme. Thus, amino acid replacements are used which form appropriate ionic and hydrophobic interactions at these points of contact. Hydrogen bonding interactions are also preferably used to identify replacements. Of course, the modelling can extend beyond the  
10           identified points of contacts in order to provide still further specificity

          This same type of analysis can be performed with the mutated cAPK that mimics the catalytic core of pp60<sup>c-src</sup>. Thus, an analysis of the mutant crystals permits one to predict the affinity of a given inhibitor. The inhibitor can be further modified to improve the ionic and hydrophobic interactions surrounding the points of contact using the spheres of  
15           influence described above. The angle of rotation of the mobile invariant residues can be used to predict whether or not a given peptide inhibitor will be useful. These changes are all performed within the constraints of the coordinates of Figure 17.

          A peptide inhibitor that, once modelled has distances similar to Table 4 and meets the design criteria described above can be synthesized and tested for function *in vitro* or *in*  
20           *vivo*.

          The coordinates obtained from the binary complex and the resulting template allow us for the first time to fully appreciate the complexity and sophistication of the process by which a protein kinase recognizes its protein substrate. While peptide analogues provide important clues, the diversity of the peptide binding sites and their dispersion over such a  
25           wide area on the enzyme surface makes it imperative to have structural data on complexes of the enzyme with effector molecules. The structure of the binary complex of cAPK with PKI(5-24) provides, for the first time, a molecular basis for the rational design of effector molecules, both peptide and nonpeptide, that can target specific protein kinases. Furthermore, because the basic catalytic core of this enzyme is so conserved in all protein  
30           kinases, a template based on the crystal structure can also serve as a mold for modelling for other protein kinases.

          Although this invention has been described using protein kinases as a model system, with cAPK being shown as a specific example of an enzyme for determining the template, the present invention is not intended to be limited to this model. Other changes to the

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methods described herein will suggest themselves to those of ordinary skill in the art. Accordingly, the spirit and scope of the present invention is to be determined with reference to the appendant claims.

**WE CLAIM:**

1. A method of designing a highly specific effector which exerts an effect on the activity of a first enzyme, said first enzyme being a member of a class of enzymes having a conserved catalytic core, comprising:

5 identifying a second enzyme that is a member of said class in which a first effector can affect the activity of said second enzyme;

forming a first complex of said first effector and said second enzyme;

10 obtaining data regarding the conformation of said second enzyme at sites greater than 5 Å from the site of catalysis of said second enzyme in said first complex;

15 designing an effector which induces a conformation on said first enzyme at sites greater than 5 Å from the site of catalysis thereof which is homologous to the conformation of the conformation of said second enzyme at homologous sites in said first complex, when said effector is formed as a second complex with said first enzyme; and

producing said effector.

2. The method of Claim 1, additionally comprising crystallizing said first complex and obtaining X-ray crystallography data therefrom.

3. The method of Claim 1, wherein the designing step comprises:

20 identifying a potential effector likely to induce a conformation on the catalytic core of said first enzyme which is homologous to the conformation of the catalytic core of said second enzyme in said first complex, when said effector is formed as a second complex with said first enzyme; and

25 determining whether said potential effector induces said conformation through the use of a technique selected from the group consisting of computer modelling, small angle neutron scattering, and circular dichroism.

4. The method of Claim 3, wherein said potential effector comprises a peptide.

30 5. The method of Claim 3, wherein said potential effector comprises a molecule selected from the group consisting of nucleotides, polynucleotides, alcohols, polymers, lipids carbohydrates, sugars, native or synthetic molecules, protein and organic compounds and combinations thereof.

6. The method of Claim 1, wherein all of the members of said class have related functions.

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7. The method of Claim 1, wherein the catalytic cores of all of the members of said class have conserved amino acid residues.

5 8. The method of Claim 7, wherein the designing step comprises designing an affector having homologous topography and charge fields that complement the catalytic core of said first enzyme and capable of inducing a conformation wherein the conserved amino acid residues of said first enzyme are in homologous locations to said second enzyme in said first complex.

9. The method of Claim 1, wherein each of the effectors is an inhibitor.

10. The method of Claims 1, wherein each of the effectors is an activator.

10 11. The method of Claim 1, wherein said first affector comprises all or a portion of said first enzyme.

12. The method of Claim 1, wherein said first complex is a holoenzyme.

13. The affector produced by the method of Claim 1.

15 14. The method of Claim 7, wherein said class of enzymes comprises protein kinases.

15. The method of Claim 14, wherein said second enzyme is a viral oncogene product or a cellular homologue thereof.

16. The method of Claim 15, wherein said second enzyme is p60 v-Src from RSV or its cellular homologue, pp60 c-src.

20 17. The method of Claim 16, wherein said second enzyme comprises cAMP-dependent protein kinase.

18. The method of Claim 2, wherein said second enzyme comprises a native mammalian protein kinase.

25 19. The method of Claim 2, wherein said second enzyme comprises recombinant protein kinase.

20. A method of designing a highly specific affector which exerts an effect on the activity of a first enzyme, said first enzyme being a member of a class of enzymes having conserved residues at an affector binding site, comprising:

30 identifying a second enzyme that is a member of said class in which a first affector can affect the activity of said second enzyme, said first affector having a dissociation constant with said second enzyme of less than 1  $\mu$ M;

forming a first complex of said first affector and said second enzyme;

obtaining data regarding the conformation of the affector binding site of said second enzyme in said first complex;



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designing an effector which induces a conformation on the effector binding site of said first enzyme which is homologous to the conformation of the effector binding site of said second enzyme in said first complex, when said effector is formed as a second complex with said first enzyme; and

5 producing said effector.

21. The method of Claim 20, wherein said class of enzymes have a nucleotide binding site and each of said effectors is capable of binding to said nucleotide binding site.

22. A method of designing a highly specific effector which exerts an effect on the activity of a first enzyme, said first enzyme being a member of a class of enzymes having a conserved catalytic core, comprising:

10 identifying a second enzyme that is a member of said class in which a first effector can affect the activity of said second enzyme;

forming a first complex of said first effector and said second enzyme, said first complex having at least three points of contact between said first effector and second enzyme;

15 obtaining data regarding the conformation of the catalytic core of said second enzyme in said first complex;

designing an effector which induces a conformation on the catalytic core of said first enzyme which is homologous to the conformation of the catalytic core of said second enzyme in said first complex, when said effector is formed as a second complex with said first enzyme; and

20 producing said effector

23. A crystallized protein kinase/effector complex having stable decay characteristics over 15 minutes.

24. A crystallized protein kinase/effector complex having a Bragg spacing diffraction limit of less than 4Å.

25. The crystallized protein kinase of Claim 24 having stable decay characteristics over 15 minutes.

26. A crystallized complex of a cAMP-dependent protein kinase and an inhibitor thereof.

27. Use of the crystallized complex of Claim 26 in an X-ray crystallography procedure to produce data regarding the three dimensional structure of said cAMP-dependent protein kinase in said complex.

28. Use of the data produced by Claim 27 for designing an inhibitor of a second protein kinase which will induce a similar three dimensional structure on the active site of said second protein kinase as the three dimensional structure of said cAMP-dependent protein kinase in said complex.

5 29. An inhibitor designed by Claim 28.

30. A method of preparing a highly specific effector of a first enzyme, said first enzyme being a member of a class of enzymes having a conserved catalytic core with a plurality of invariant residues, comprising:

- 10 a. identifying a second enzyme that is a member of said class and having a known effector thereof;
- b. forming a first complex of said second enzyme and said known effector;
- c. obtaining data regarding the three dimensional coordinates of said invariant residues in said first complex, said coordinates forming a template;
- 15 d. generating a model wherein said first enzyme is in a conformation in which said invariant residues are in substantially the same conformation as in said template;
- e. identifying a change in the variable residues in the catalytic core of said first enzyme in the conformation of step (d) when compared to the variable residues in the catalytic core of said second enzyme in the conformation of step (b);
- 20 f. preparing a modified form of said second enzyme, wherein the modified second enzyme includes the non-conserved change identified in step (e);
- g. designing an effector which computer modelling indicates will induce a conformation on the catalytic core of said first enzyme in which said invariant residues are in substantially the same coordinates as the coordinates of said template, when said first enzyme is formed as a second complex with the effector designed in this step; and
- 25 h. producing said effector.

30 31. The method of Claim 30 wherein said change is a non-conserved change in the variable residues.

32. The method of Claim 30, additionally comprising:

- i. forming a third complex of said modified second enzyme and an effector capable of binding thereto;

j. obtaining data regarding the three dimensional coordinates of the invariant residues in said third complex; and

k. using the data obtained in step (i) to design an affector which computer modelling indicates will induce a conformation on the catalytic core of said first enzyme in which said invariant residues are closer to the coordinates of said template than the conformation induced by the affector designed in step (g), when said first enzyme is formed as a fourth complex with the affector designed in this step.

33. The method of Claim 32 wherein the affector of step (i) is the known affector of step (a).

34. The method of Claim 32, additionally comprising modifying the computer modelling used in step (g) in light of the data of step (j), prior to performing step (k).

35. The method of Claim 30, additionally comprising obtaining amino acid sequence data relating to the catalytic cores of the first and second enzymes.

36. The method of Claim 30 wherein step (f) comprises site directed mutagenesis of a recombinantly produced second enzyme.

37. The method of Claim 30, wherein the coordinates of said template are substantially as shown in Figure 17.

38. The method of Claim 30, wherein each of the effectors is an inhibitor.

39. The method of Claim 30, wherein said template includes coordinates separated by the distances substantially as shown in Table 4.

40. An affector prepared by the method of Claim 39.

41. A pharmaceutical composition comprising the affector of Claim 40.

42. A method of designing a specific inhibitor for a protein kinase, comprising: obtaining data regarding the three-dimensional structure of a first protein kinase;

using said data in the design of an inhibitor for a second, different, protein kinase; and

producing said inhibitor.

43. The method of Claim 42 wherein said first protein kinase is cAMP dependent protein kinase or an analogue thereof.

44. The method of Claim 43, wherein the obtaining step comprises crystallizing a complex of cAMP dependent protein kinase and an inhibitor thereof.

45. The method of Claim 44, wherein the obtaining step additionally comprises obtaining X-ray crystallography data on the crystallized complex obtained from the crystallizing step.

5 46. The method of Claim 44, additionally comprising obtaining information regarding the structure of the crystallized complex obtained in the crystallizing step through circular dichroism, small angle neutron scattering, or other chemical procedures.

47. Use of the data of Figure 17 or of Table 4 in the design of an affector for a protein kinase.

10 48. A method of preparing a highly specific inhibitor of a first enzyme, said first enzyme being a member of a class of enzymes having a conserved catalytic core with a plurality of invariant residues, comprising:

a. identifying a second enzyme that is a member of said class and having a known first inhibitor thereof;

b. forming a first complex of said second enzyme and said first inhibitor;

15 c. obtaining data regarding the three dimensional coordinates of said invariant residues in said first complex;

d. designing a second inhibitor which computer modelling indicates will induce a conformation on the catalytic core of said first enzyme in which said invariant residues are in substantially the same coordinates as the coordinates obtained in step (c), when said first enzyme is formed as a second complex with said second inhibitor;

e. preparing said second inhibitor;

25 f. forming a third complex of said second inhibitor and a third enzyme complexable therewith, said third enzyme having a plurality of said invariant residues;

g. obtaining data regarding the three dimensional coordinates of said invariant residues in said third complex;

30 h. using the data obtained from step (g) to design a third inhibitor which computer modelling indicates will induce a conformation on the catalytic core of said first enzyme closer to that in which said invariant residues are in substantially the same coordinates as the coordinates obtained in step (c) than induced by the second inhibitor, when said first enzyme is formed as a fourth complex with said third inhibitor; and

i. producing said third inhibitor.

49. The method of Claim 48, wherein said first inhibitor is an inhibitory domain of said second enzyme.

50. The method of Claim 48, wherein said third enzyme comprises at least 5 invariant residues.

5 51. The method of Claim 48, wherein said third enzyme is a naturally occurring enzyme.

52. The method of Claim 48, wherein said third enzyme is a mutant enzyme.

10 53. A method of determining the efficacy of a first effector in affecting a first enzyme that is a member of a class of enzymes having a plurality of invariant residues among the members of said class, comprising:

determining the three dimensional coordinates of the invariant residues of a second enzyme in a first conformation wherein said second enzyme is in a complex with a second effector that is a strong effector of said enzyme;

15 determining the three dimensional coordinates of the invariant residues of said second enzyme in a second conformation wherein said enzyme is in a conformation other than said first conformation;

identifying the mobile invariant residues of said enzyme, said mobile invariant residues being those invariant residues at coordinates substantially different in said first conformation than in said second conformation;

20 determining the three dimensional coordinates of the mobile invariant residues of said first enzyme when said first enzyme is in a conformation wherein said first enzyme is in a complex with said first effector;

25 comparing the three dimensional coordinates of the mobile invariant residues of said first enzyme in said conformation with the coordinates of the mobile invariant residues of said enzyme in said first conformation, wherein relatively small differences in the coordinates indicate relatively high efficacy of said first effector.

54. The method of Claim 53, wherein the step of determining the coordinates of said first enzyme in said conformation is performed using computer modelling of said conformation.

30 55. The method of Claim 53, wherein the steps of determining the first and second conformations comprise obtaining X-ray crystallographic data of said enzyme.

56. The method of Claim 53, wherein said second conformation is a conformation produced by a ternary complex.



57. The method of Claim 56, wherein said ternary complex comprises a protein kinase, a nucleotide and an effector.

58. The method of Claim 53, wherein said second conformation is a conformation produced by said second enzyme not complexed with a ligand.

5 59. The method of Claim 53, wherein said second enzyme is the same enzyme as said first enzyme.

60. A method of designing specific inhibitors of a first protein kinase having a template defined by a plurality of invariant residues present in substantially all protein kinases, comprising:

10 obtaining data regarding the three dimensional coordinates of the invariant residues of a second protein kinase and of the points of contact between said second protein kinase and a known inhibitor thereof, said coordinates being obtained when said second protein kinase is formed as a complex with said known inhibitor;

15 generating a model of said first protein complex wherein said template is defined by the positions of said invariant residues in said complex;

examining the amino acid residues present in said first protein kinase at positions corresponding to the points of contact in said complex;

designing an inhibitor of said first protein kinase capable of forming ionic and hydrophobic interactions with said amino acid residues; and

20 producing said inhibitor of said first protein kinase.

61. The method of Claim 60, wherein said second protein kinase is cAMP dependent protein kinase.

62. The method of Claim 61, wherein said known inhibitor is PKI(5-24).

25 63. The method of Claim 62, wherein the points of contact in said complex comprise positions corresponding to the positions selected from the group consisting of P+1, P-2, P-3, P-6 and P-11 along said known inhibitor.

64. The method of Claim 60, wherein the positions corresponding to the points of contact in the examining step comprise positions within a sphere having a radius of 11 Å from the coordinates of the point of contact obtained in the obtaining step.

30 65. The method of Claim 64, wherein the positions corresponding to the points of contact in the examining step comprise positions within a sphere having a radius of 6 Å from the coordinates of the point of contact obtained in the obtaining step.

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66. The method of Claim 60, wherein the designing step additionally comprises designing said inhibitor to form appropriate hydrogen bonding with said amino acid residues.

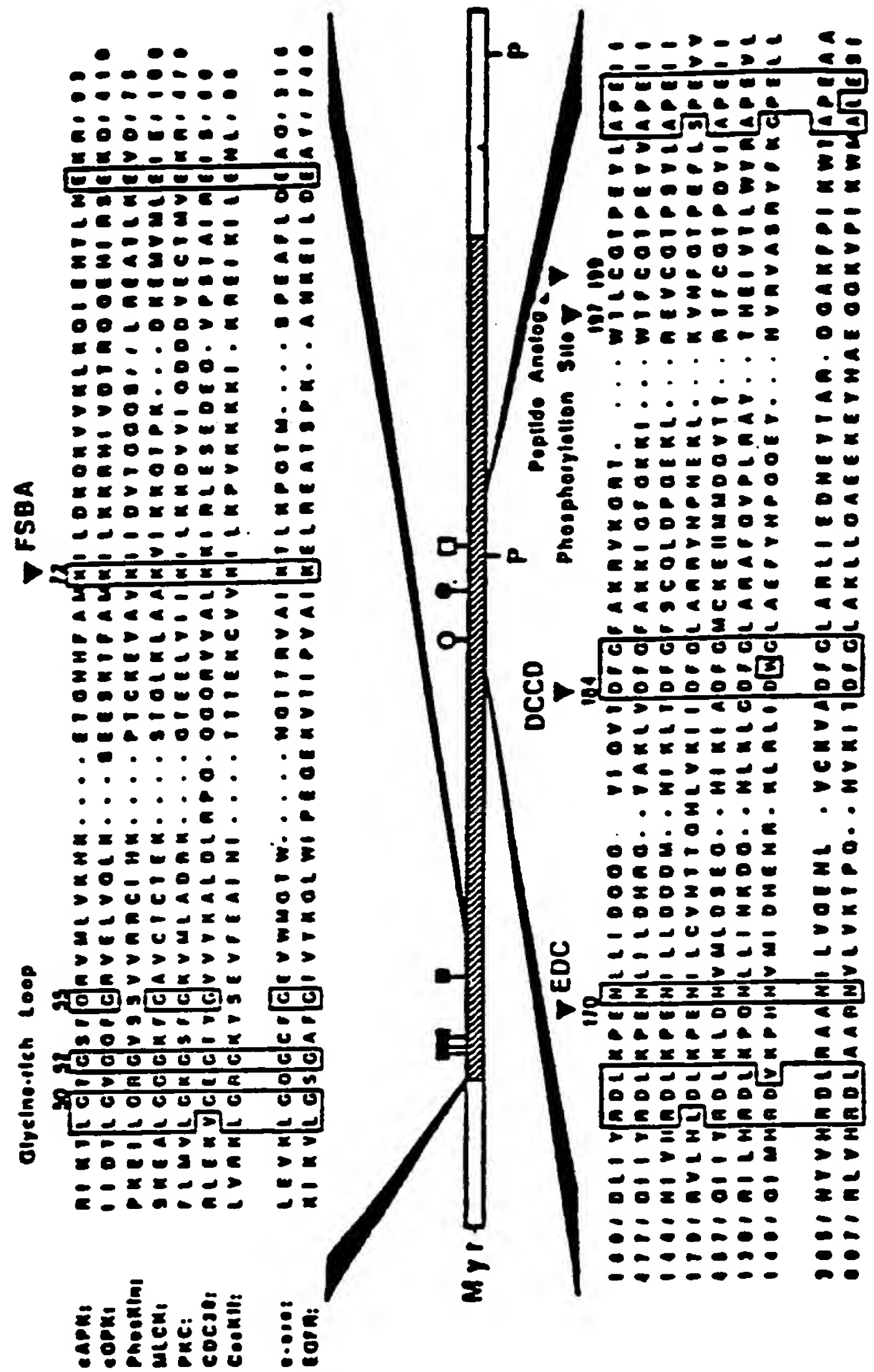
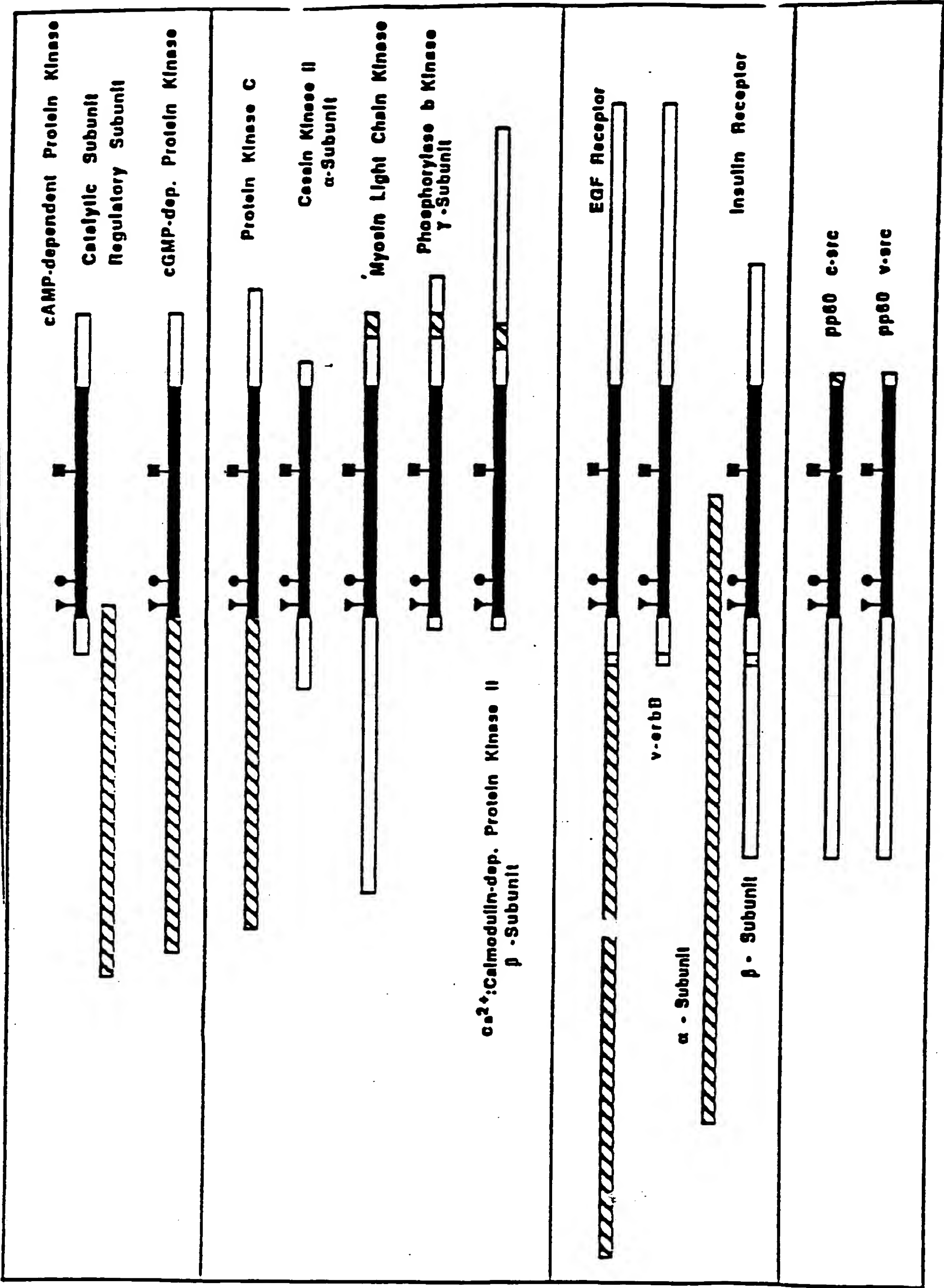


FIGURE 2



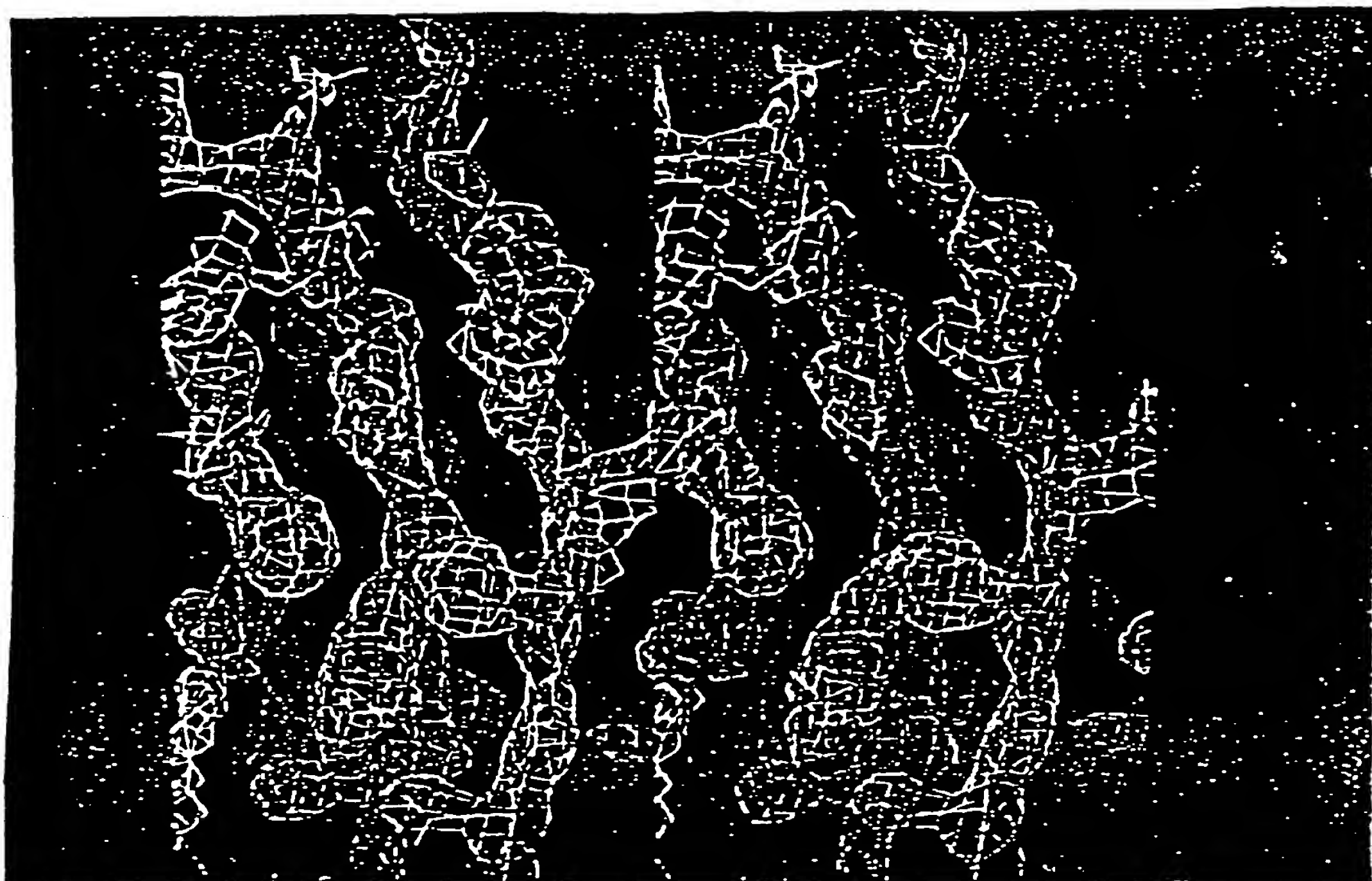


FIGURE 3A

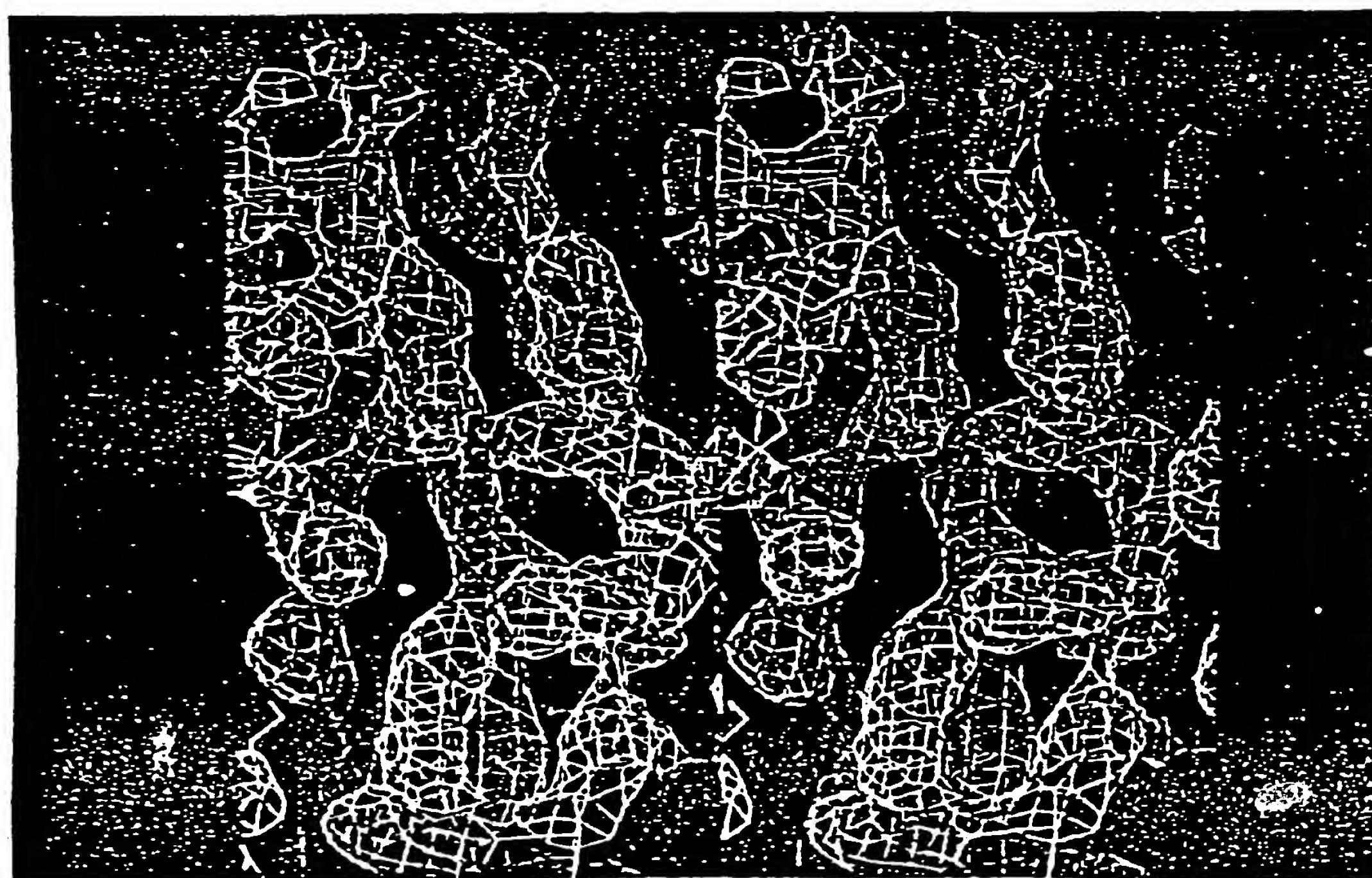
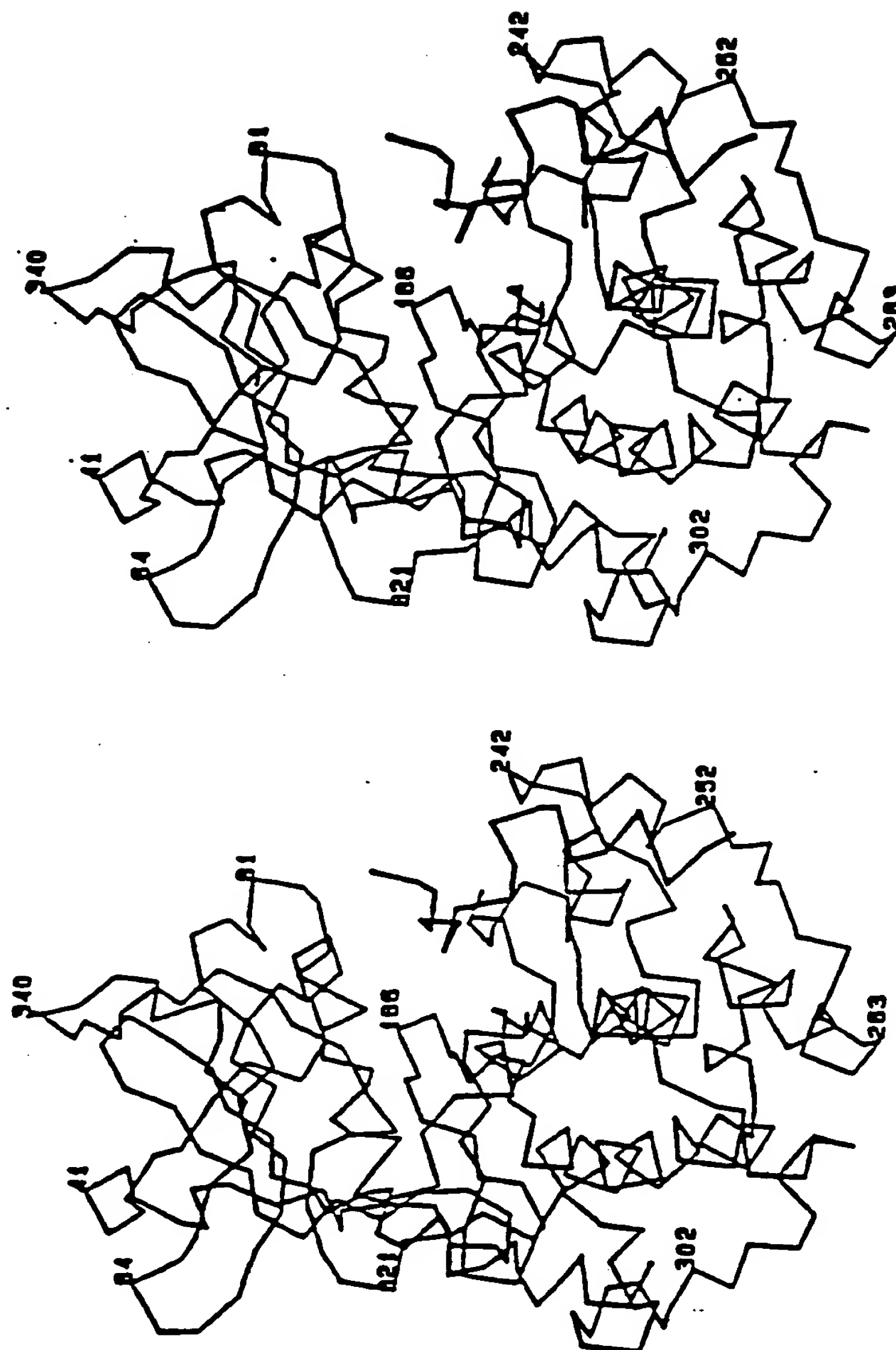


FIGURE 3B

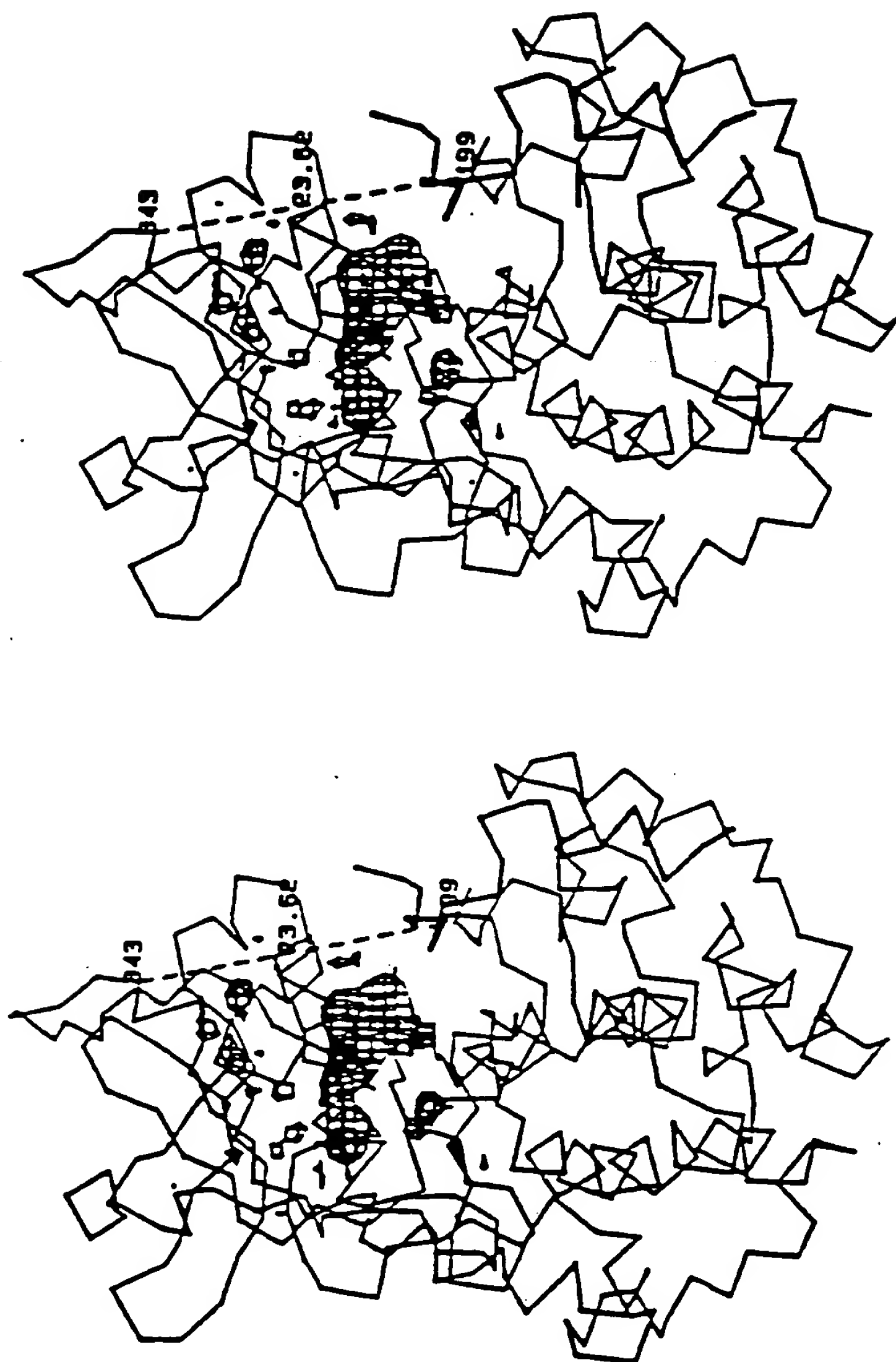


FIGURE 4



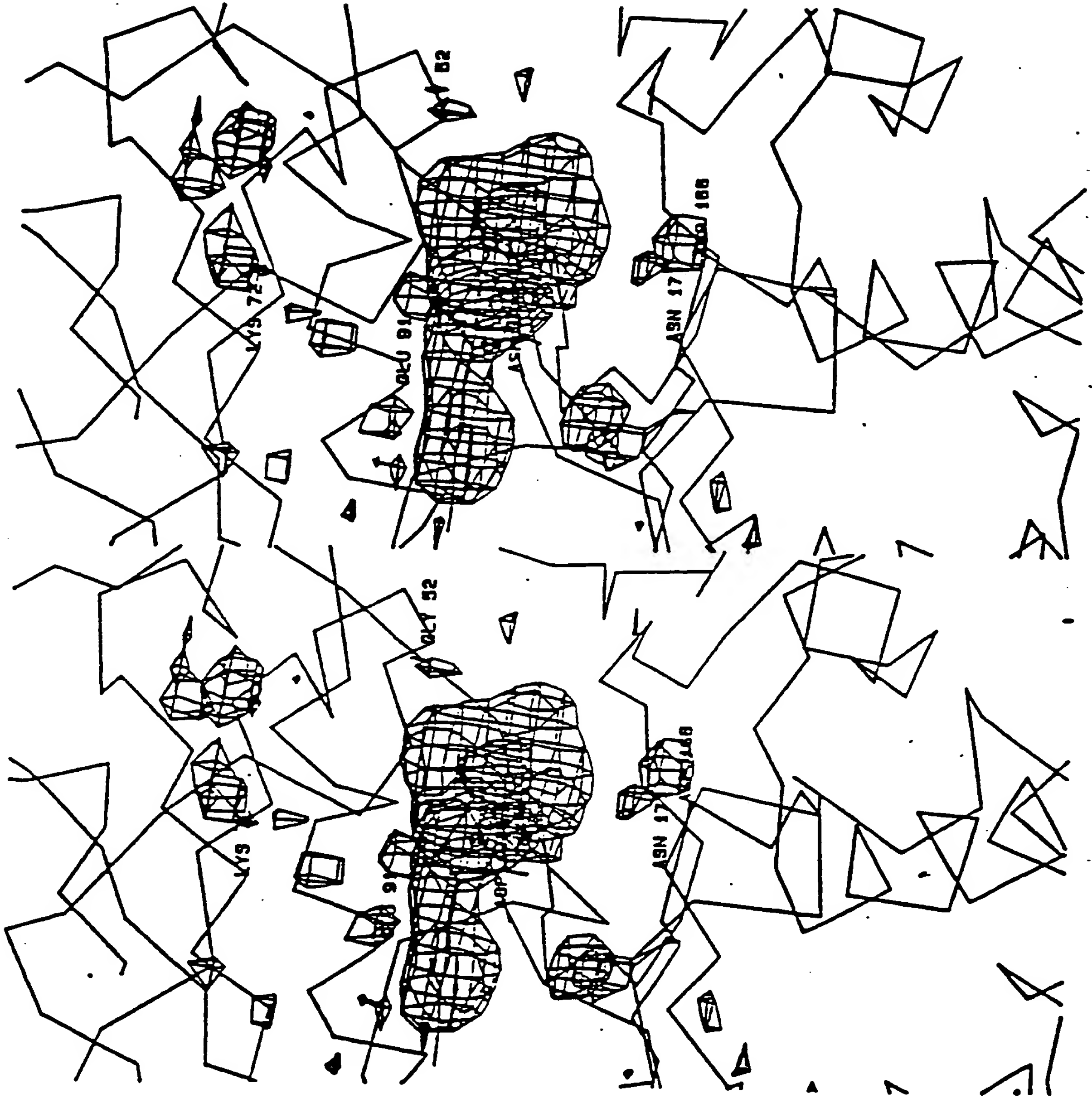
5/49

FIGURE 5A

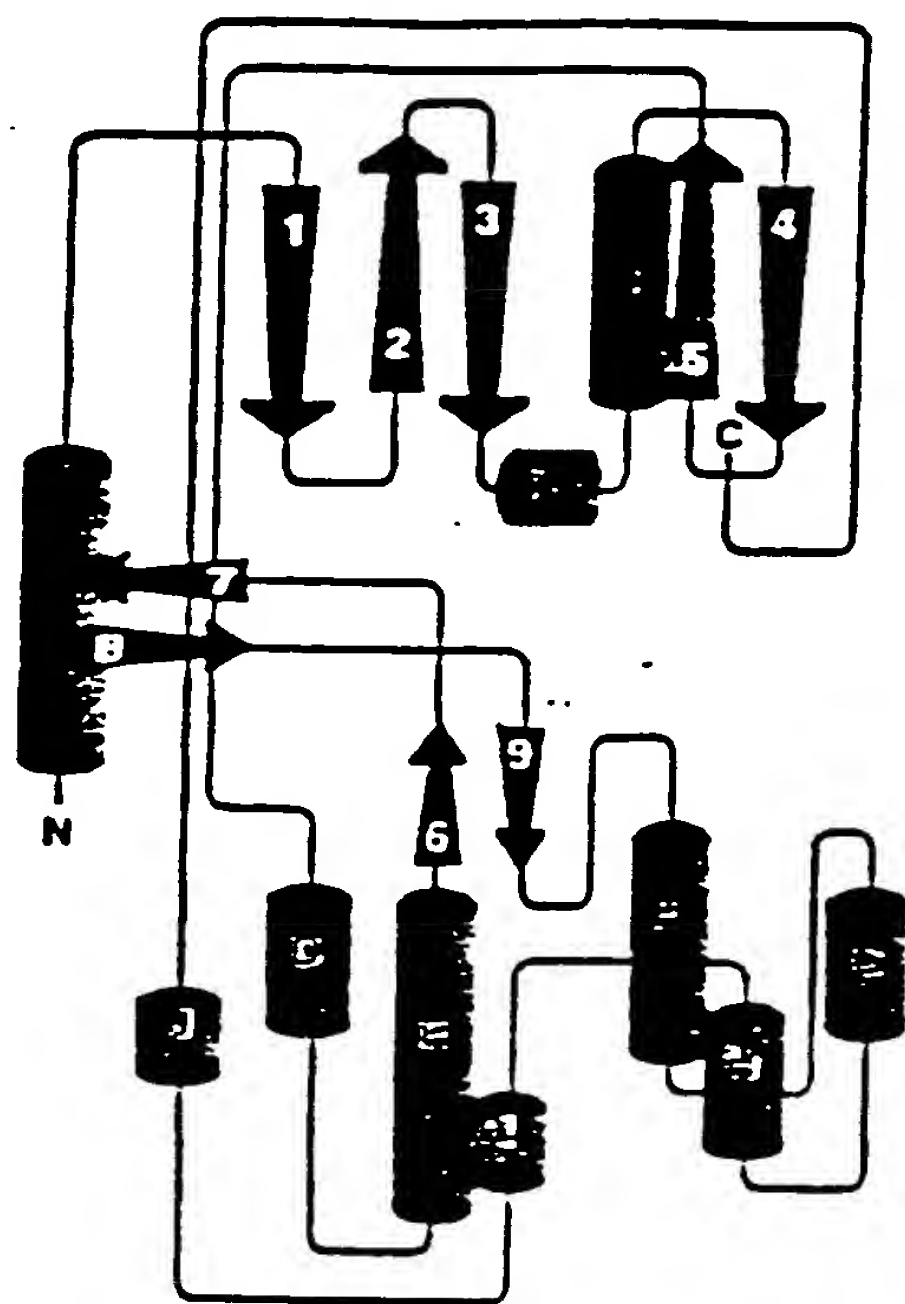


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FIGURE 5B



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FIGURE

6

FIGURE 7B

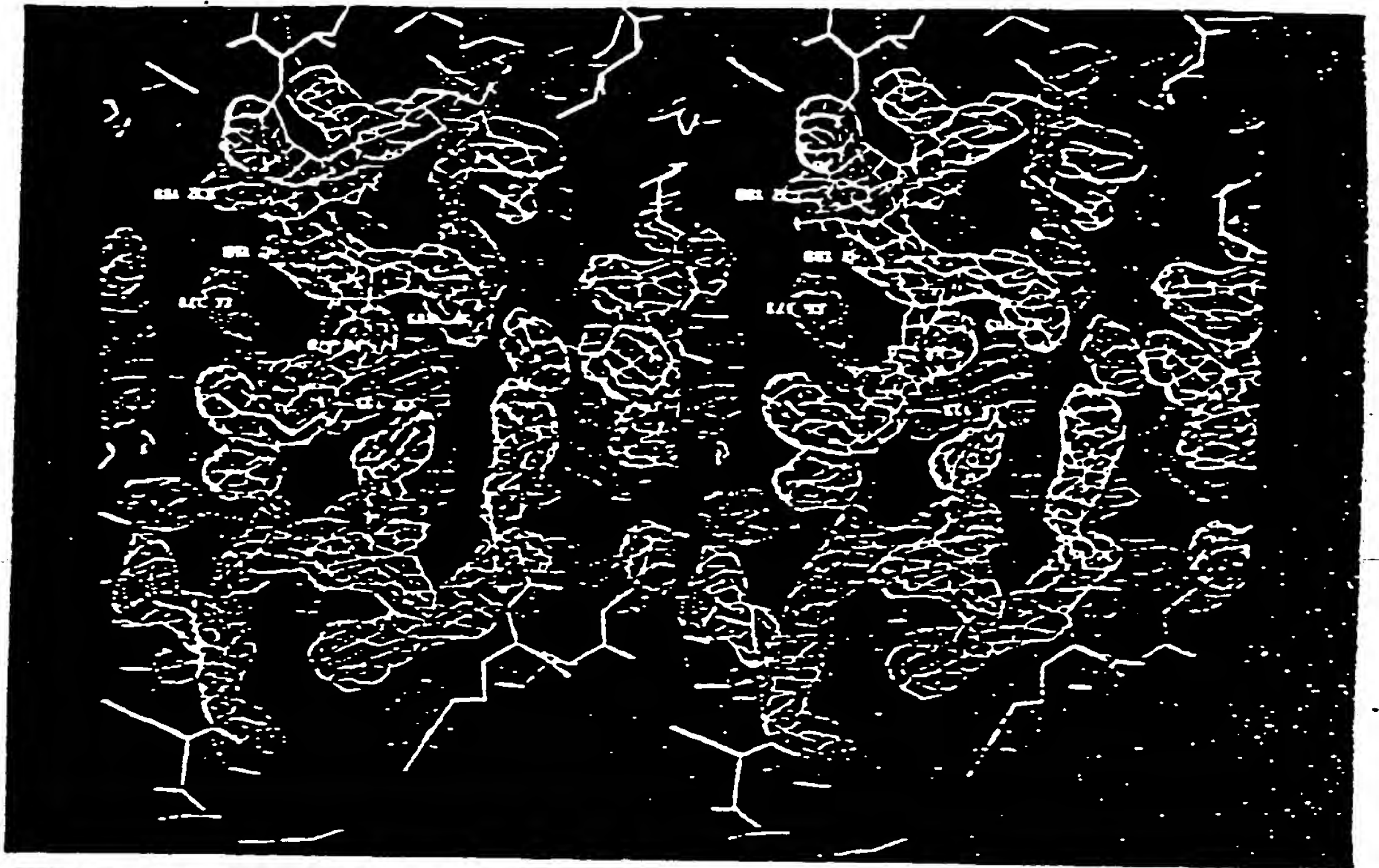
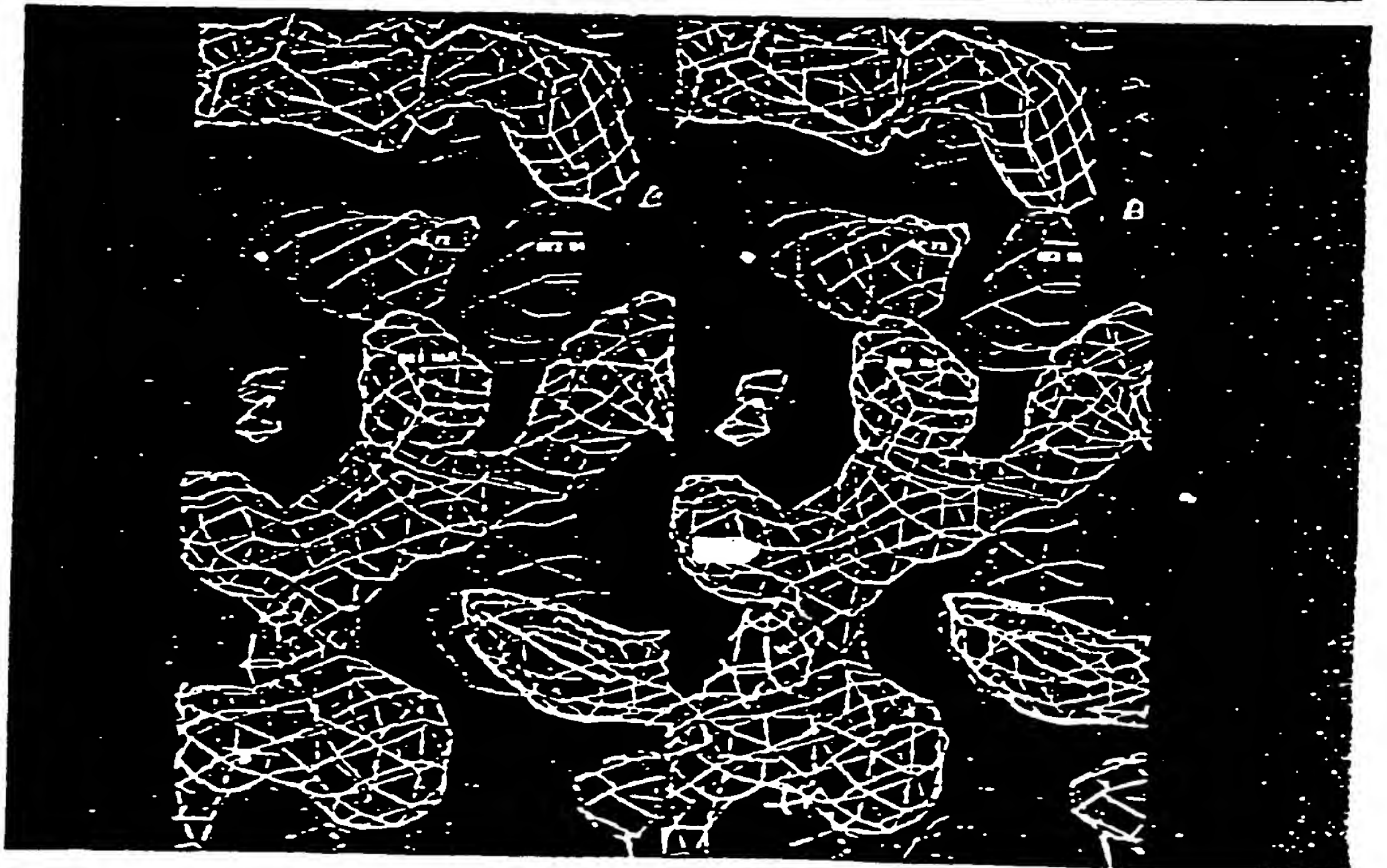
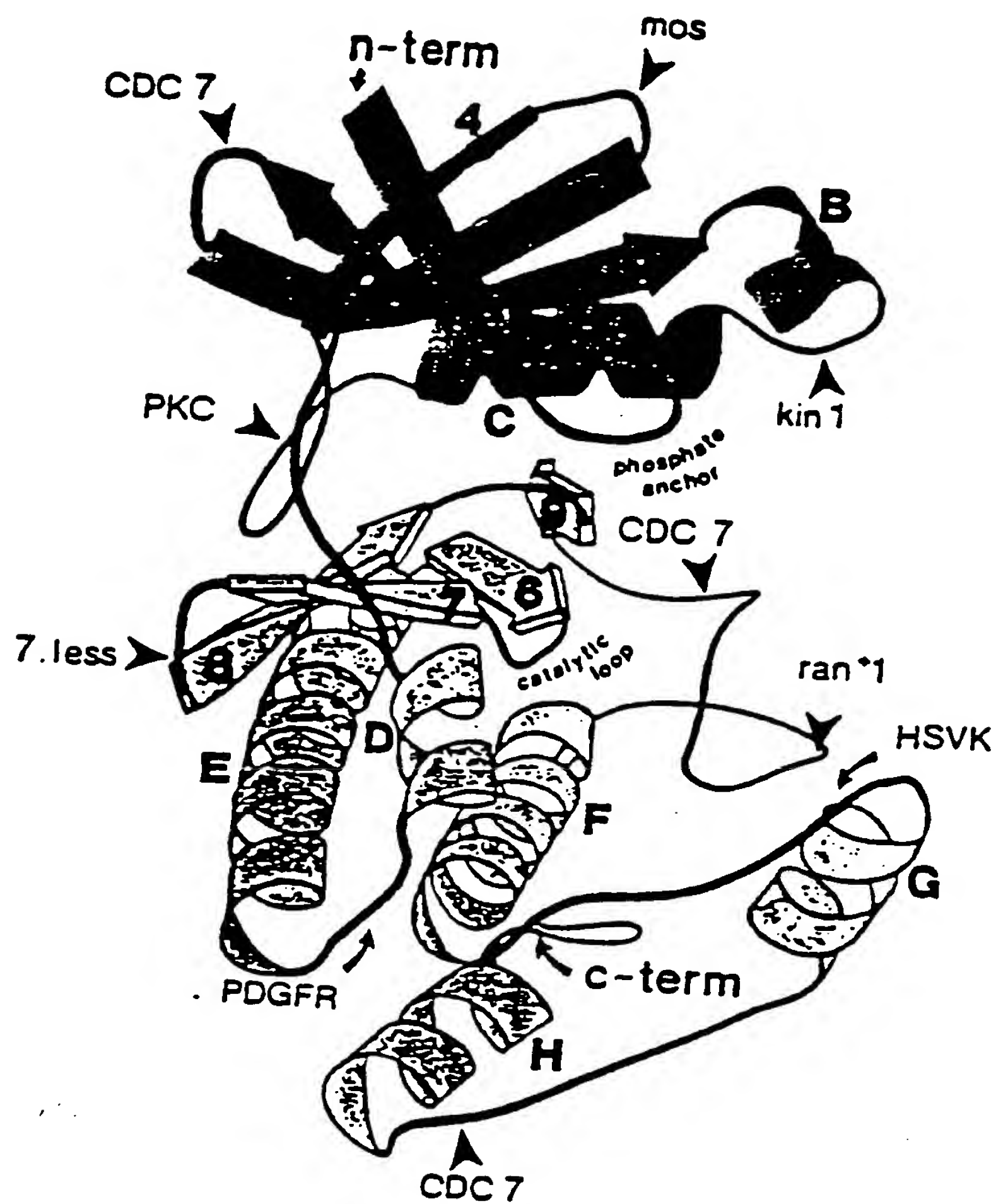


FIGURE 7A





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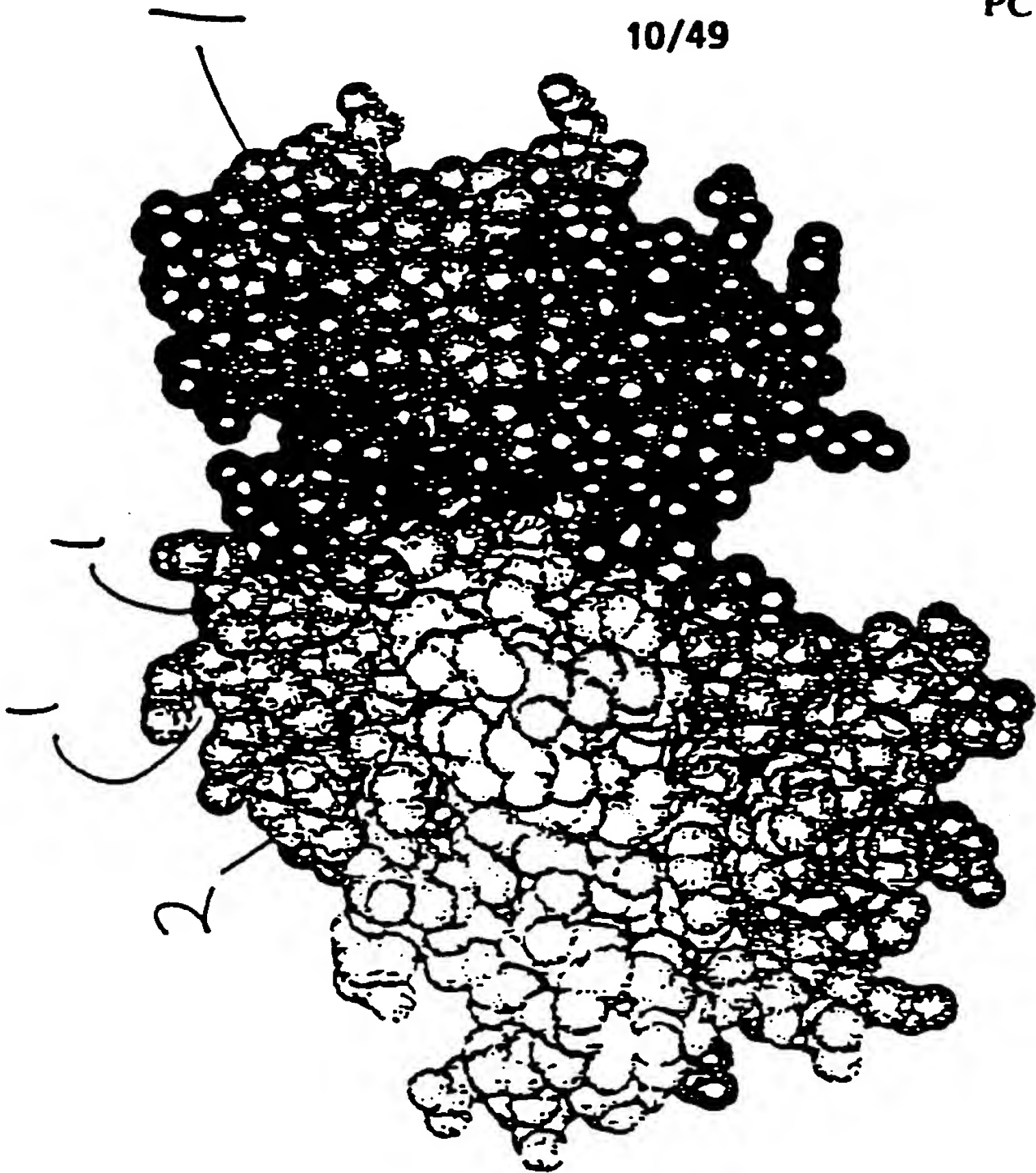


FIGURE

8B

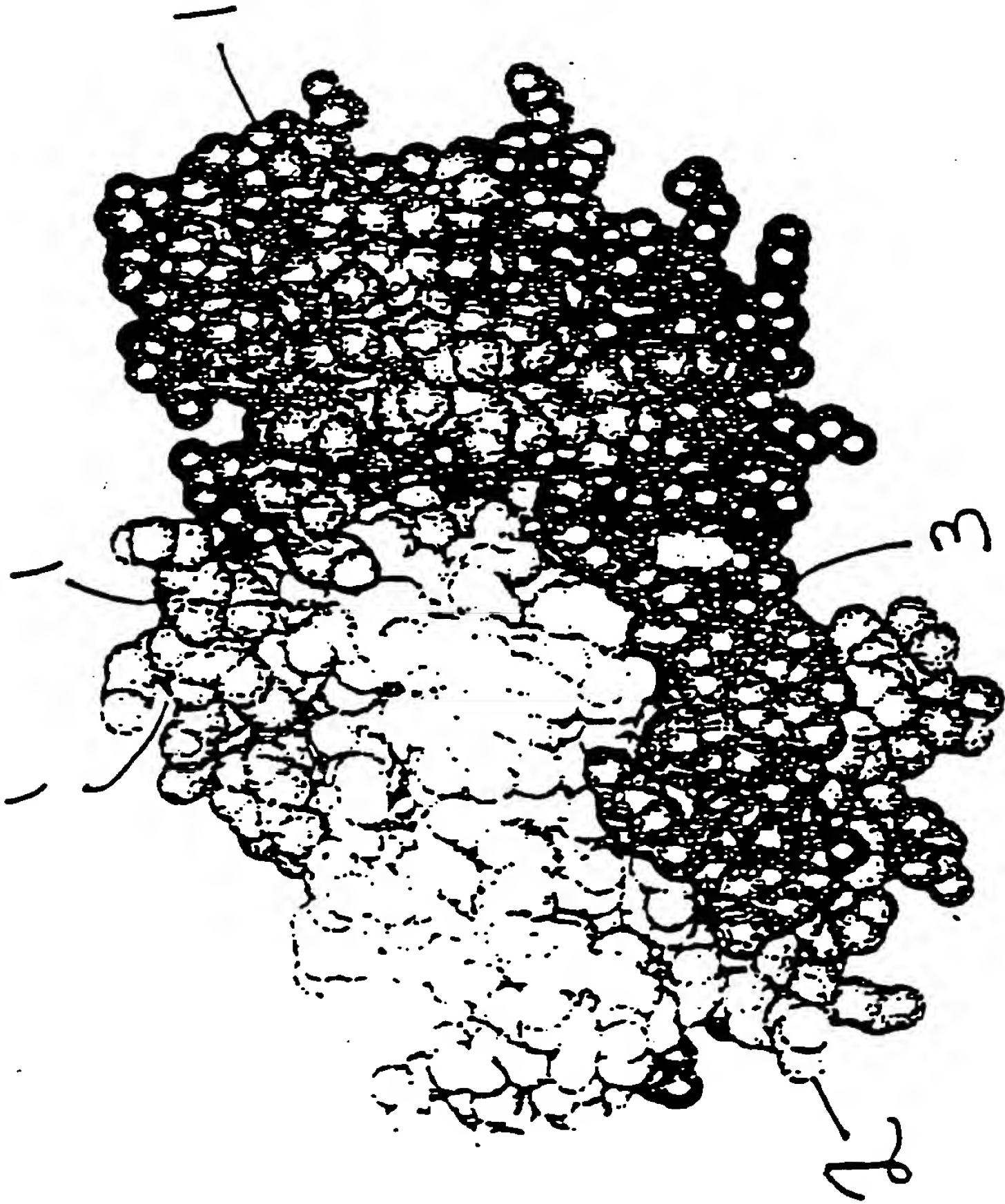
8A

FIGURE



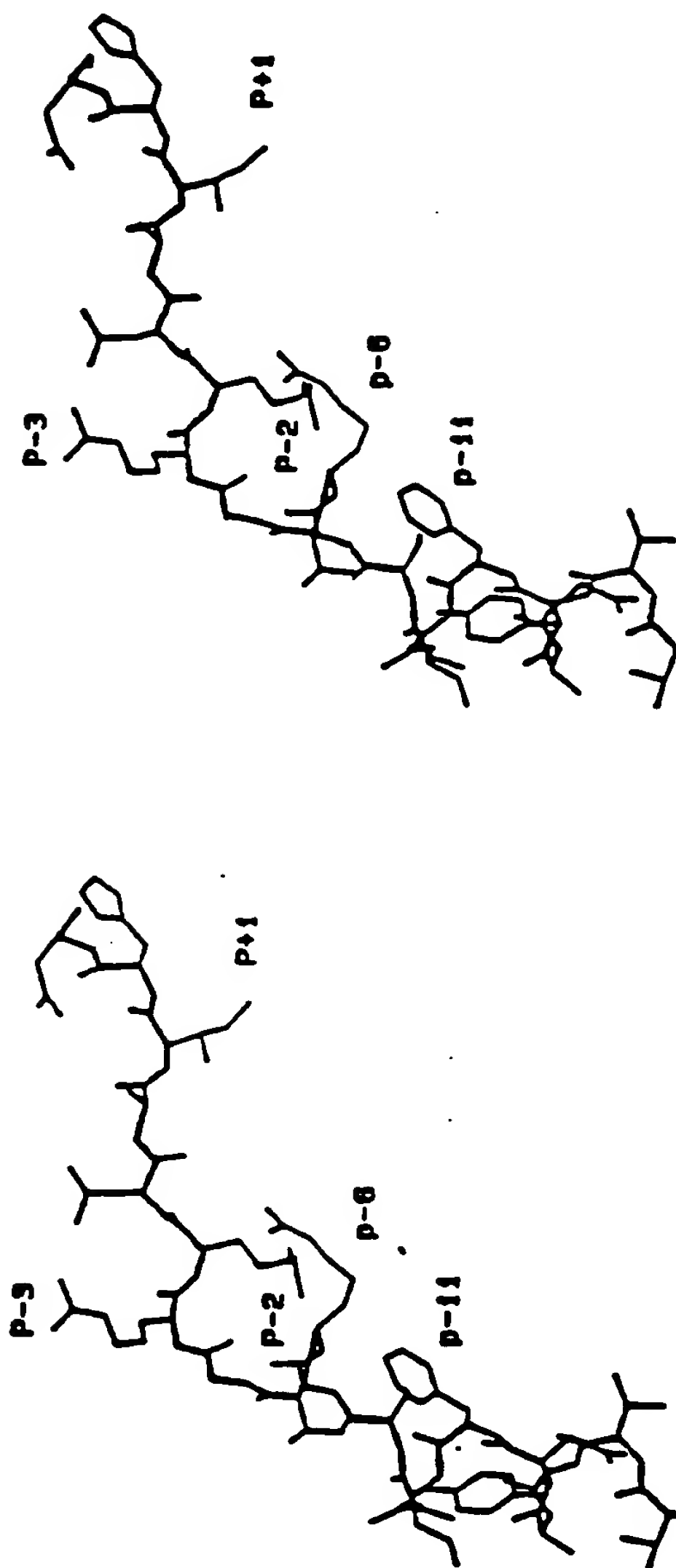
8C

FIGURE



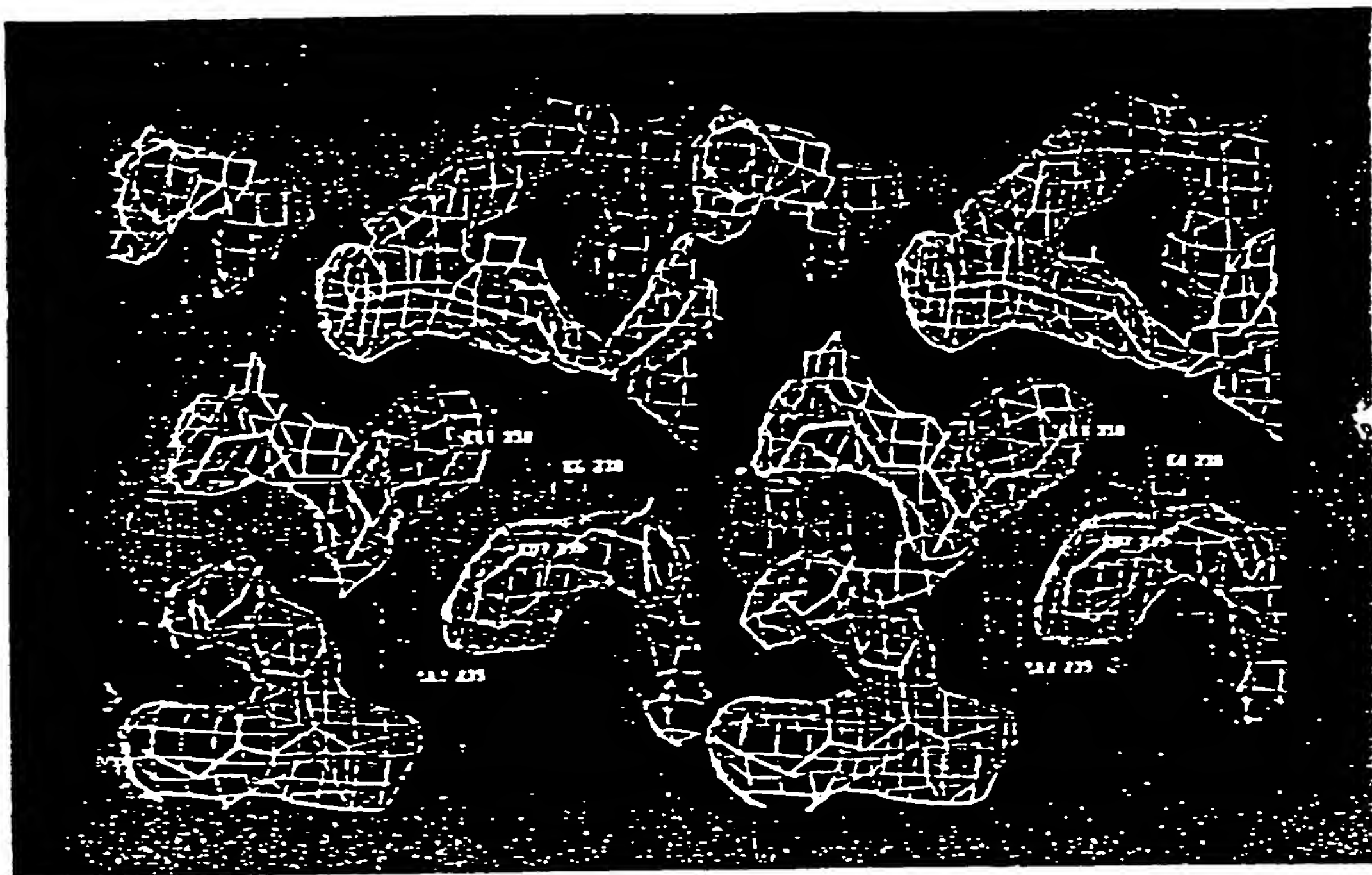
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FIGURE 9



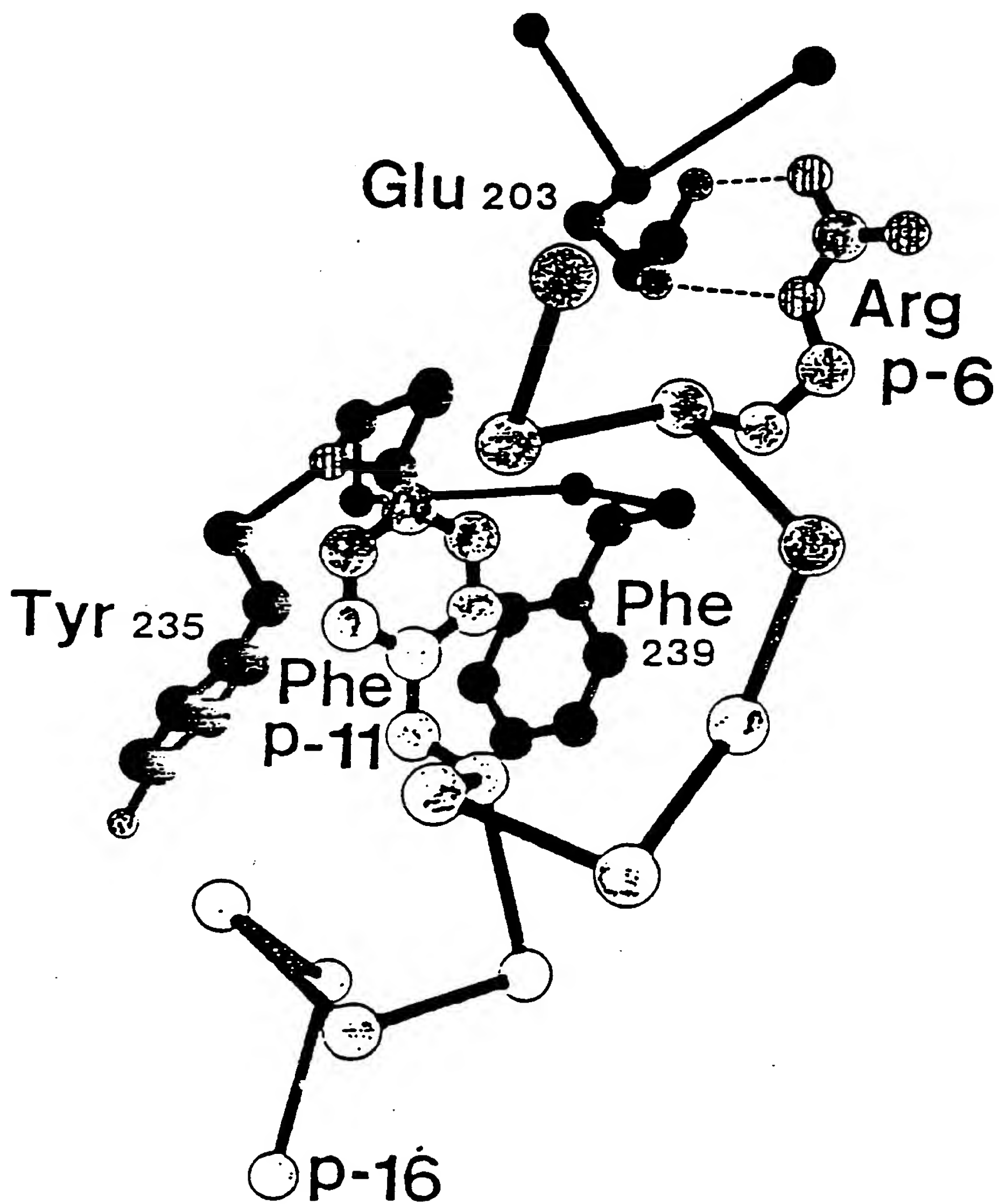
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FIGURE 10A



FIGURE

10B





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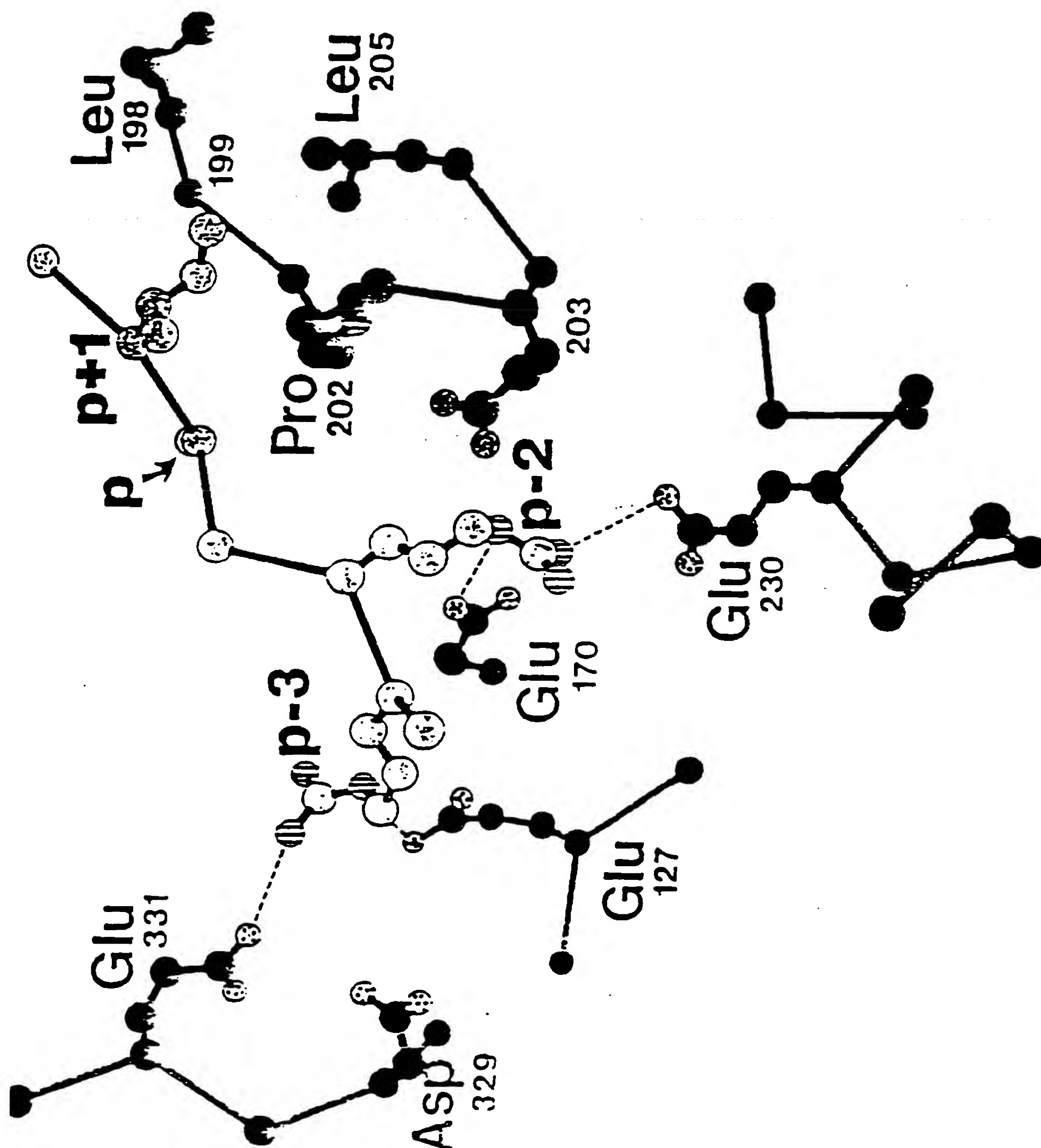


FIGURE 11

FIGURE 12B

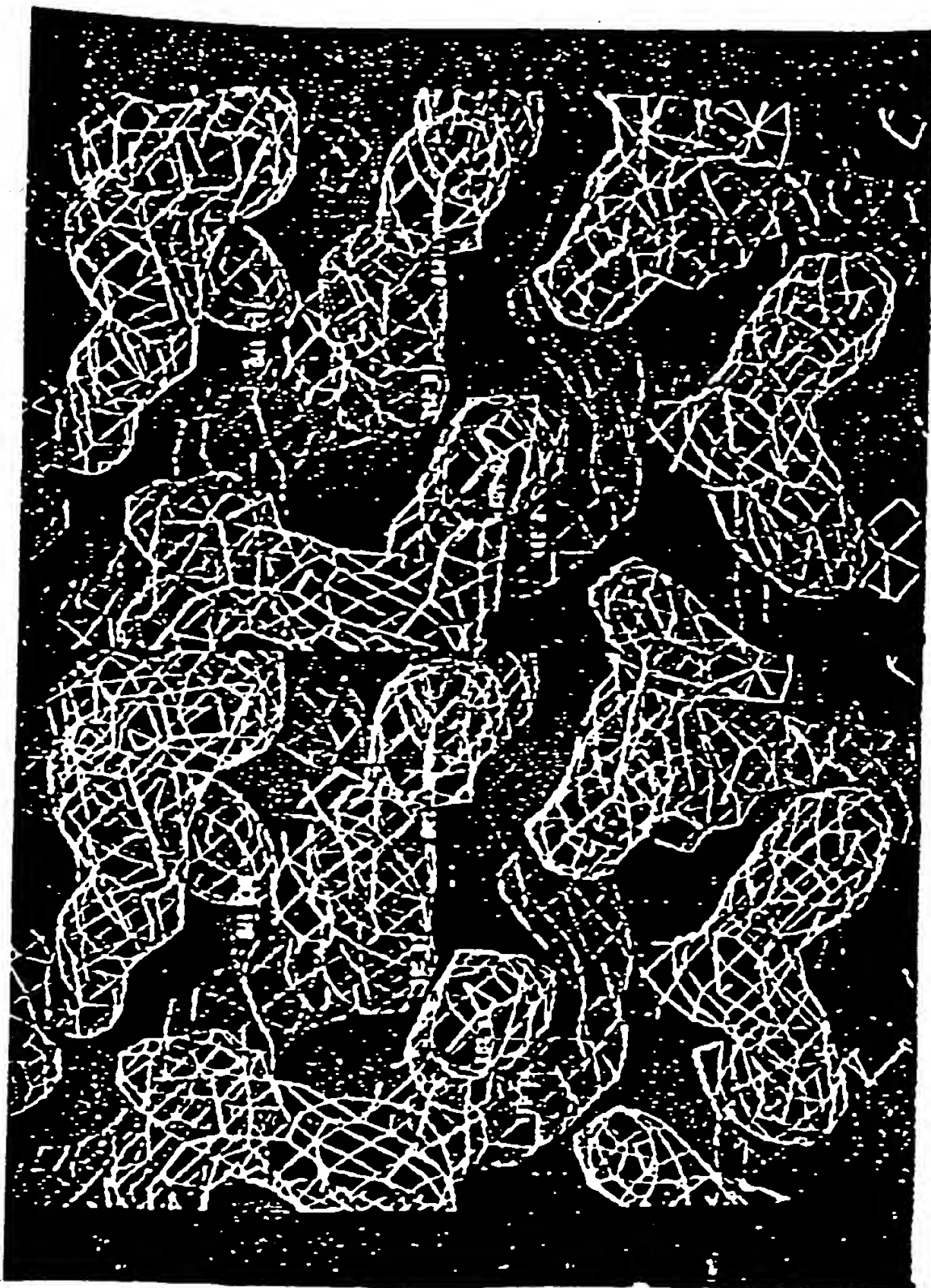


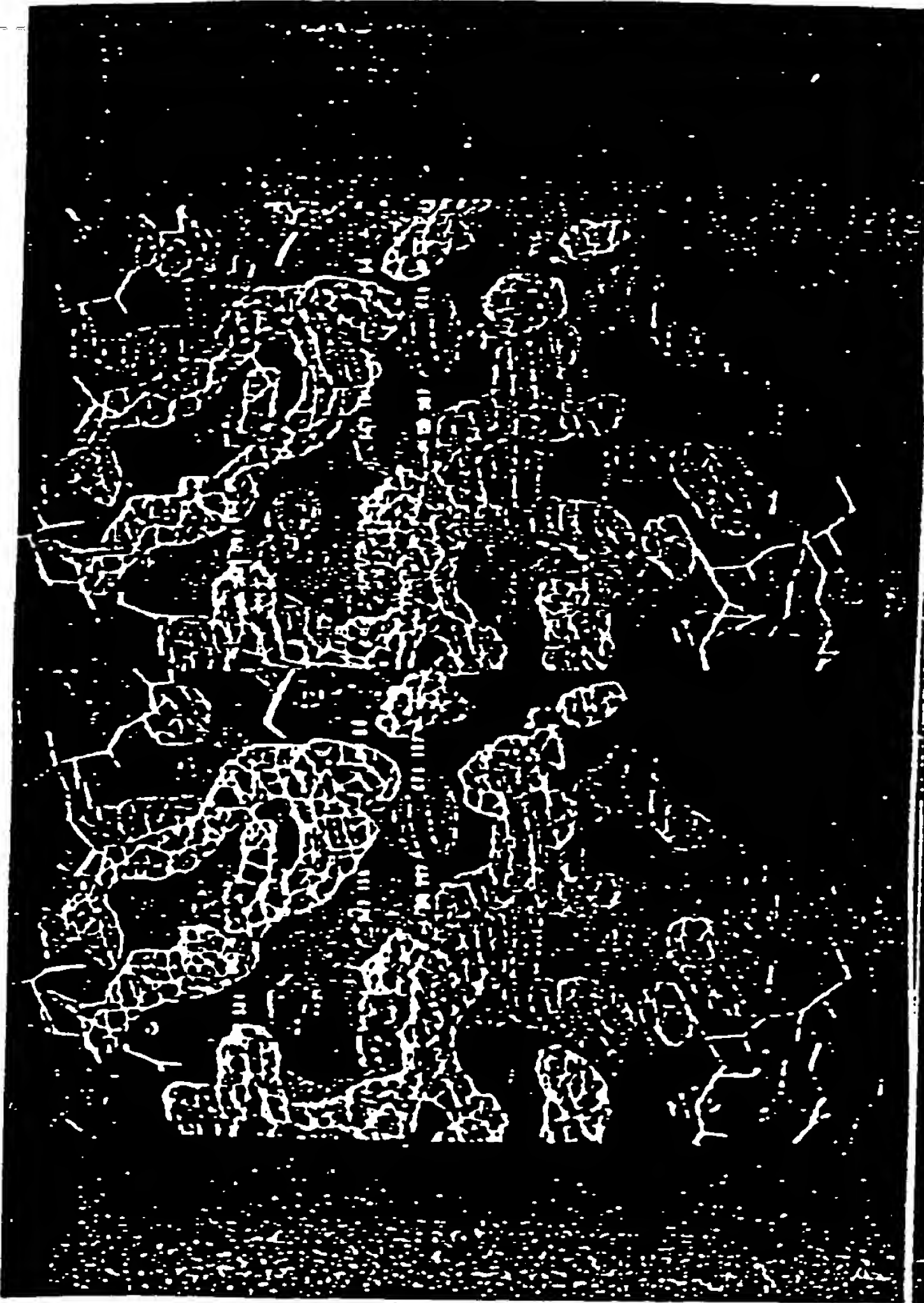
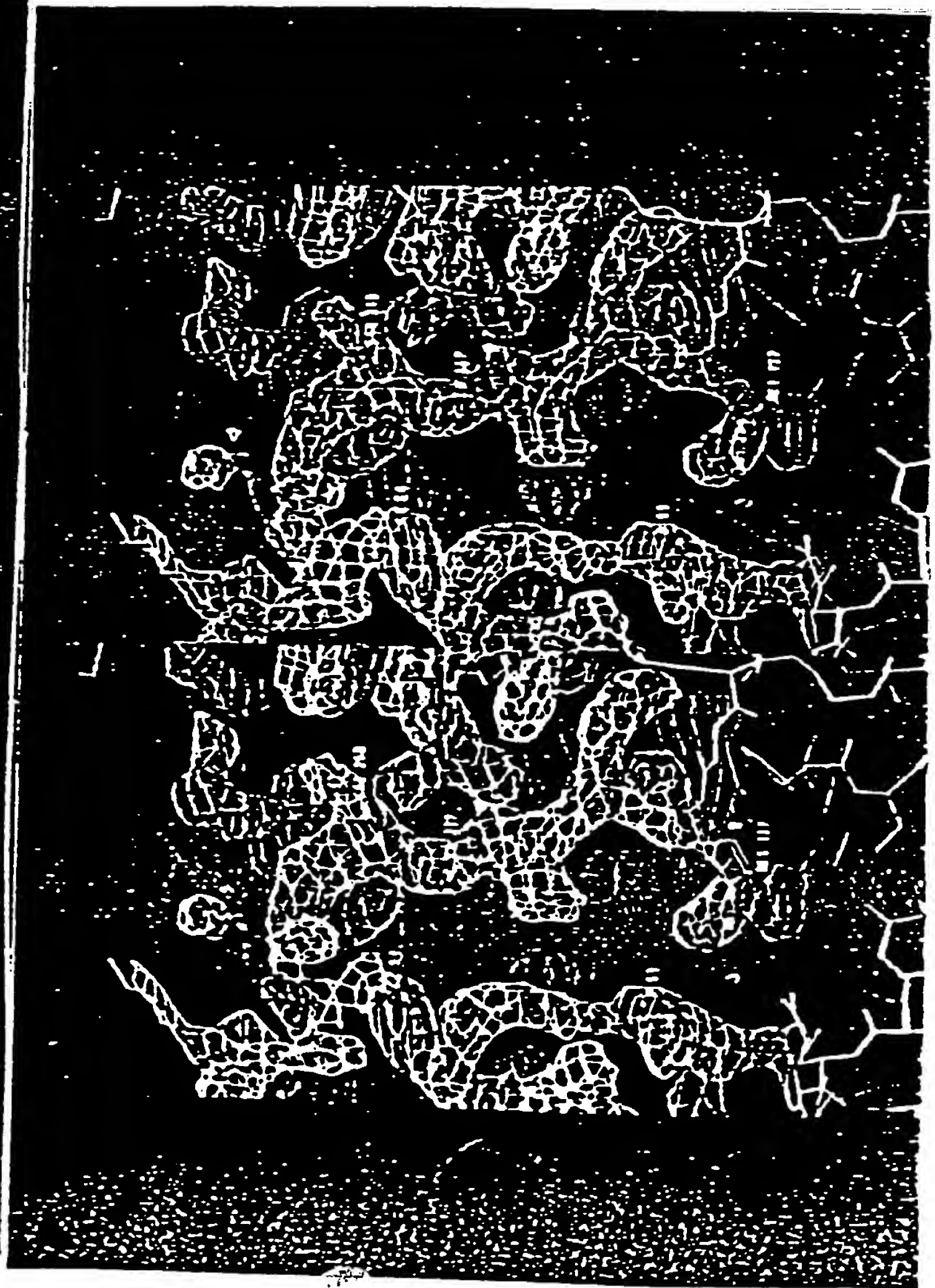
FIGURE 12A



FIGURE 12C



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FIGURE  
13AFIGURE  
13B



13C

FIGURE



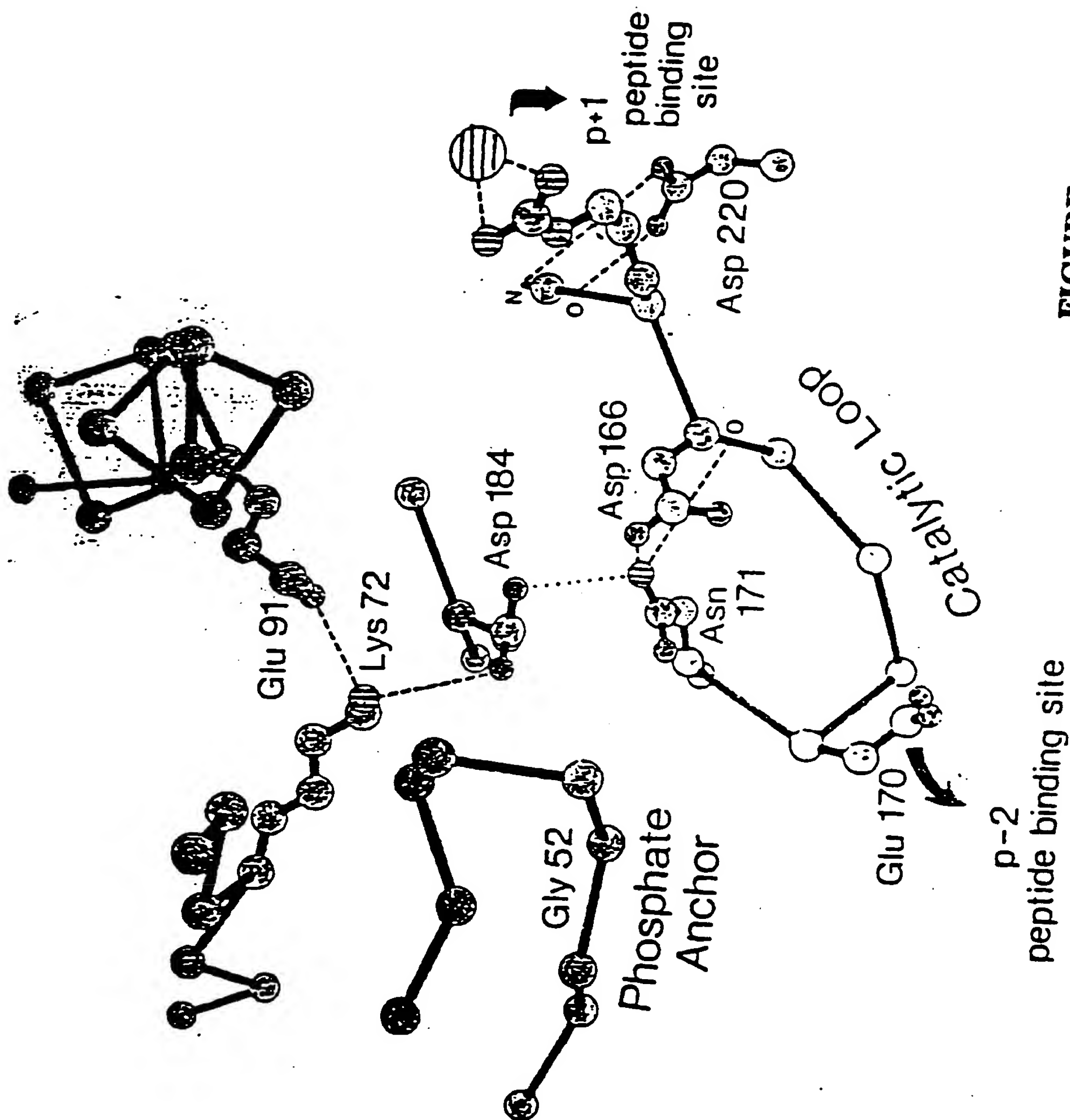
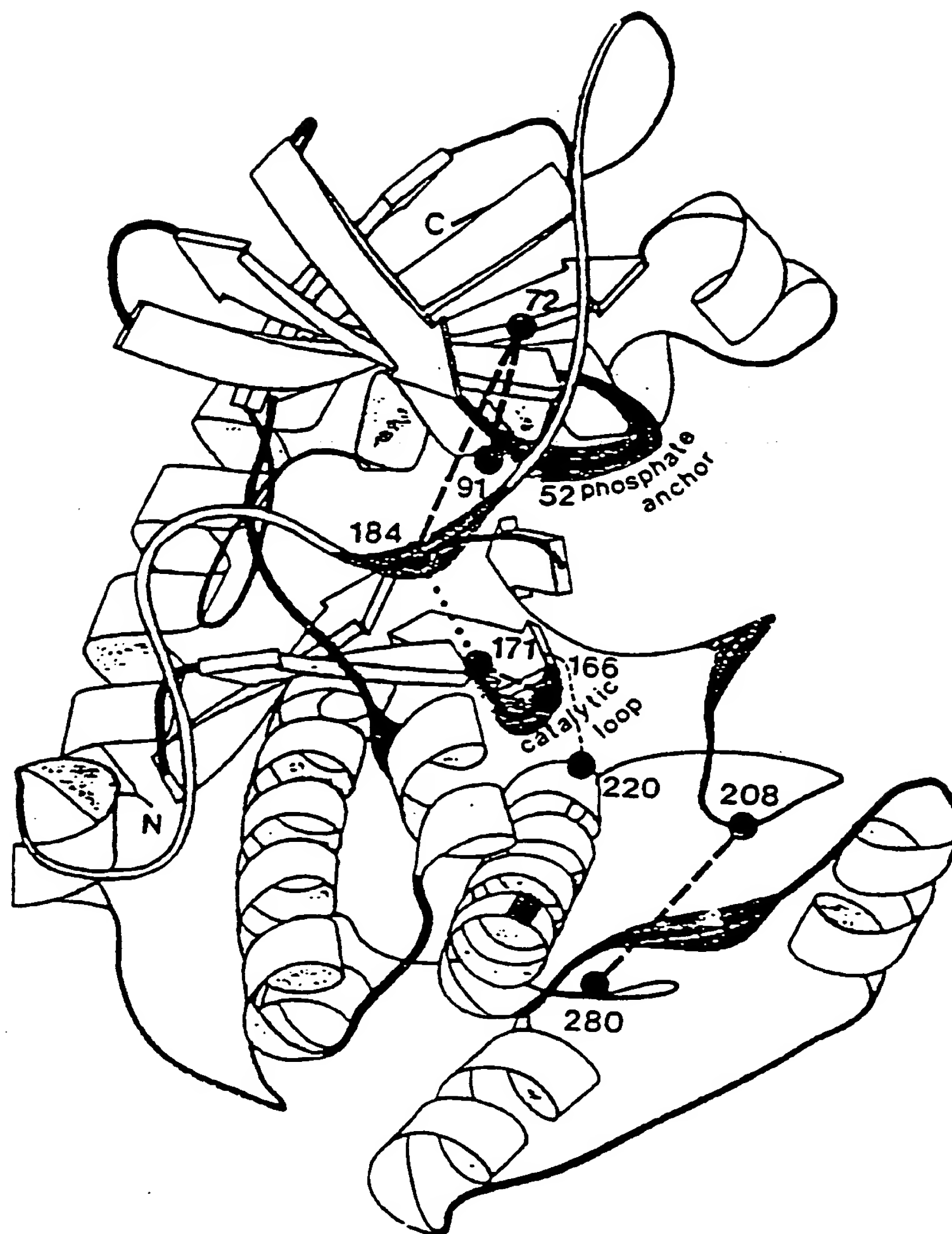


FIGURE 14



FIGURE

15

FIGURE 16

PKI(5-24)

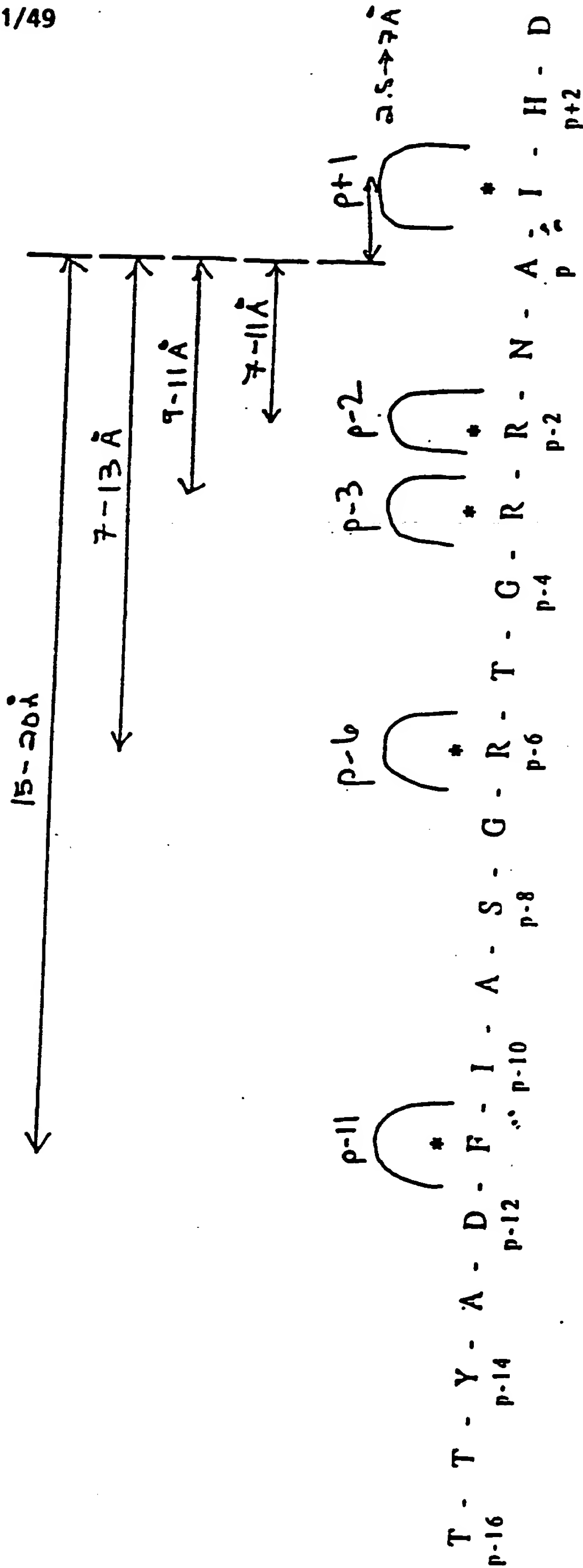


FIGURE 17

Coordinates of Catalytic Subunit of cAMP-dependent Protein Kinase (Residues 35-350) Complexed with PKI(3-24) (Residues 331-370)

(Residues 331-350) Complexed with PKI(31-24) (Residues 331-370)																								
ATOM	1	N	VAL	15	-5.333	-10.224	-32.585	1.00	17.60	ATOM	63	O	ALA	22	-3.283	0.697	-17.114	1.00	17.60					
ATOM	2	CA	VAL	15	-3.967	-10.703	-33.261	1.00	17.60	ATOM	64	K	LYS	23	-3.215	-1.311	-18.109	1.00	17.60					
ATOM	3	CB	VAL	15	-3.226	-12.101	-33.183	1.00	17.60	ATOM	65	CA	LYS	23	-2.294	-0.925	-19.116	1.00	17.60					
ATOM	4	CG1	VAL	15	-1.737	-11.768	-33.430	1.00	17.60	ATOM	66	CB	LYS	23	-2.360	-2.006	-20.164	1.00	17.60					
ATOM	5	CG2	VAL	15	-3.523	-12.950	-33.871	1.00	17.60	ATOM	67	CG	LYS	23	-0.874	-2.829	-20.085	1.00	17.60					
ATOM	6	C	VAL	15	-4.211	-10.316	-34.716	1.00	17.60	ATOM	68	CD	LYS	23	0.264	-2.286	-21.013	1.00	17.60					
ATOM	7	O	VAL	15	-4.787	-9.210	-34.806	1.00	17.60	ATOM	69	CE	LYS	23	1.564	-2.361	-20.830	1.00	17.60					
ATOM	8	N	LYS	16	-3.916	-11.110	-35.767	1.00	17.60	ATOM	70	NE	LYS	23	2.770	-2.680	-21.509	1.00	17.60					
ATOM	9	CA	LYS	16	-6.109	-10.950	-37.248	1.00	17.60	ATOM	71	C	LYS	23	-2.733	0.347	-19.782	1.00	17.60					
ATOM	10	CB	LYS	16	-6.590	-12.205	-37.900	1.00	17.60	ATOM	72	O	LYS	23	-2.080	1.383	-19.778	1.00	17.60					
ATOM	11	CG	LYS	16	-3.763	-13.627	-37.732	1.00	17.60	ATOM	73	N	GLU	24	-3.999	0.273	-20.268	1.00	17.60					
ATOM	12	CD	LYS	16	-4.563	-16.710	-38.529	1.00	17.60	ATOM	74	CA	GLU	24	-4.471	1.361	-21.034	1.00	17.60					
ATOM	13	CE	LYS	16	-6.104	-16.178	-38.613	1.00	17.60	ATOM	75	C3	GLU	24	-5.708	0.950	-21.060	1.00	17.60					
ATOM	14	NE	LYS	16	-4.304	-16.378	-38.613	1.00	17.60	ATOM	76	CO	GLU	24	-5.518	0.187	-23.234	1.00	17.60					
ATOM	15	C	LYS	16	-5.113	-17.140	-38.063	1.00	17.60	ATOM	77	CD	GLU	24	-5.260	1.099	-24.554	1.00	17.60					
ATOM	16	O	LYS	16	-5.101	-9.015	-37.609	1.00	17.60	ATOM	78	OE1	GLU	24	-6.038	0.872	-25.539	1.00	17.60					
ATOM	17	N	GLU	17	-6.845	-8.788	-38.115	1.00	17.60	ATOM	79	OE2	GLU	24	-4.271	1.788	-24.609	1.00	17.60					
ATOM	18	CA	GLU	17	-6.223	-10.208	-37.038	1.00	17.60	ATOM	80	C	GLU	24	-4.763	2.572	-20.331	1.00	17.60					
ATOM	19	CB	GLU	17	-7.386	-9.372	-36.928	1.00	17.60	ATOM	81	O	GLU	24	-4.713	3.583	-20.917	1.00	17.60					
ATOM	20	CO	GLU	17	-8.277	-10.817	-35.723	1.00	17.60	ATOM	82	N	ASP	25	-5.034	2.715	-18.923	1.00	17.60					
ATOM	21	CD	GLU	17	-7.484	-10.689	-34.607	1.00	17.60	ATOM	83	CA	ASP	25	-5.354	6.311	-18.475	1.00	17.60					
ATOM	22	OE1	GLU	17	-8.290	-11.406	-33.533	1.00	17.60	ATOM	84	CO	ASP	25	-5.172	6.311	-18.475	1.00	17.60					
ATOM	23	OE2	GLU	17	-6.492	-12.620	-33.634	1.00	17.60	ATOM	85	CO	ASP	25	-6.081	4.402	-17.197	1.00	17.60					
ATOM	24	C	GLU	17	-6.704	-10.738	-32.578	1.00	17.60	ATOM	86	OD1	ASP	25	-6.753	5.833	-17.305	1.00	17.60					
ATOM	25	O	GLU	17	-7.374	-7.872	-36.681	1.00	17.60	ATOM	87	OD2	ASP	25	-7.180	6.224	-18.412	1.00	17.60					
ATOM	26	N	PHE	18	-7.072	-7.008	-37.561	1.00	17.60	ATOM	88	C	ASP	25	-3.776	4.616	-18.172	1.00	17.60					
ATOM	27	CA	PHE	18	-7.012	-7.590	-35.393	1.00	17.60	ATOM	89	O	ASP	25	-3.317	3.814	-18.335	1.00	17.60					
ATOM	28	CB	PHE	18	-7.103	-6.244	-34.915	1.00	17.60	ATOM	90	N	PHE	26	-2.819	3.492	-17.828	1.00	17.60					
ATOM	29	CG	PHE	18	-7.518	-6.403	-33.459	1.00	17.60	ATOM	91	CA	PHE	26	-3.433	4.056	-17.608	1.00	17.60					
ATOM	30	CD1	PHE	18	-7.323	-5.308	-32.709	1.00	17.60	ATOM	92	CB	PHE	26	-0.463	3.849	-17.432	1.00	17.60					
ATOM	31	CD2	PHE	18	-7.725	-3.995	-32.998	1.00	17.60	ATOM	93	CG	PHE	26	0.935	3.360	-17.127	1.00	17.60					
ATOM	32	CE1	PHE	18	-6.073	-5.310	-31.808	1.00	17.60	ATOM	94	CD1	PHE	26	1.312	3.093	-15.886	1.00	17.60					
ATOM	33	CE2	PHE	18	-7.241	-2.867	-32.354	1.00	17.60	ATOM	95	CD2	PHE	26	1.900	3.393	-18.112	1.00	17.60					
ATOM	34	CE	PHE	18	-5.593	-6.220	-31.164	1.00	17.60	ATOM	96	CE1	PHE	26	-0.463	4.461	-15.614	1.00	17.60					
ATOM	35	C	PHE	18	-6.100	-7.982	-31.442	1.00	17.60	ATOM	97	CE2	PHE	26	3.122	3.915	-17.068	1.00	17.60					
ATOM	36	O	PHE	18	-5.358	-5.614	-35.366	1.00	17.60	ATOM	98	CE	PHE	26	3.319	4.198	-16.636	1.00	17.60					
ATOM	37	N	LEU	19	-6.702	-6.424	-35.497	1.00	17.60	ATOM	99	C	PHE	26	-1.013	4.781	-18.065	1.00	17.60					
ATOM	38	CA	LEU	19	-3.473	-5.82	-35.499	1.00	17.60	ATOM	100	O	PHE	26	-0.778	5.989	-18.014	1.00	17.60					
ATOM	39	CB	LEU	19	-3.384	-6.913	-35.303	1.00	17.60	ATOM	101	N	LEU	27	-1.033	6.181	-20.014	1.00	17.60					
ATOM	40	CG	LEU	19	-1.390	-6.499	-34.424	1.00	17.60	ATOM	102	CA	LEU	27	-0.489	6.835	-21.202	1.00	17.60					
ATOM	41	CD1	LEU	19	-1.617	-8.126	-33.015	1.00	17.60	ATOM	103	CB	LEU	27	-0.510	3.907	-22.403	1.00	17.60					
ATOM	42	CD2	LEU	19	-0.232	-7.664	-34.368	1.00	17.60	ATOM	104	CG	LEU	27	0.637	3.887	-22.666	1.00	17.60					
ATOM	43	C	LEU	19	-3.392	-5.214	-36.930	1.00	17.60	ATOM	105	CD1	LEU	27	1.089	3.119	-21.440	1.00	17.60					
ATOM	44	O	LEU	19	-2.456	-6.478	-37.346	1.00	17.60	ATOM	106	CD2	LEU	27	0.103	1.787	-23.556	1.00	17.60					
ATOM	45	N	ALA	20	-4.187	-5.517	-37.658	1.00	17.60	ATOM	107	C	LEU	27	-1.203	6.118	-21.510	1.00	17.60					
ATOM	46	CA	ALA	20	-4.700	-5.823	-38.918	1.00	17.60	ATOM	108	O	LEU	27	-0.552	7.024	-22.015	1.00	17.60					
ATOM	47	CB	ALA	20	-5.381	-6.062	-39.811	1.00	17.60	ATOM	109	N	LYS	28	-3.435	6.307								

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ATOM	128	CA	TRP	30	1.608	8.431	-19.347	1.00	17.60	ATOM	193	C	THR	37	-1.725	22.256	-9.221	1.00	17.60
ATOM	129	CB	TRP	30	1.945	7.029	-19.784	1.00	17.60	ATOM	194	O	THR	37	-2.481	23.703	-9.315	1.00	17.60
ATOM	130	CO	TRP	30	3.397	6.084	-20.380	1.00	17.60	ATOM	195	N	ALA	38	-3.009	22.080	-8.107	1.00	17.60
ATOM	131	CD	TRP	30	4.475	6.972	-19.343	1.00	17.60	ATOM	196	CA	ALA	38	-1.278	22.965	-6.309	1.00	17.60
ATOM	132	CE	TRP	30	5.509	6.989	-20.257	1.00	17.60	ATOM	197	CB	ALA	38	-1.037	22.231	-5.708	1.00	17.60
ATOM	133	CE	TRP	30	4.737	7.062	-18.000	1.00	17.60	ATOM	198	C	ALA	38	-0.460	24.243	-6.977	1.00	17.60
ATOM	134	CD	TRP	30	3.726	6.003	-21.497	1.00	17.60	ATOM	199	O	ALA	38	0.331	24.564	-7.997	1.00	17.60
ATOM	135	NE	TRP	30	5.025	6.805	-21.497	1.00	17.60	ATOM	200	N	GLN	39	-0.399	25.033	-5.897	1.00	17.60
ATOM	136	CE	TRP	30	6.828	7.111	-19.865	1.00	17.60	ATOM	201	CA	GLN	39	0.532	26.157	-5.813	1.00	17.60
ATOM	137	CE	TRP	30	6.056	7.182	-17.587	1.00	17.60	ATOM	202	CB	GLN	39	-0.171	27.351	-6.332	1.00	17.60
ATOM	138	CH	TRP	30	7.089	7.212	-18.503	1.00	17.60	ATOM	203	CG	GLN	39	0.431	28.749	-6.308	1.00	17.60
ATOM	139	C	TRP	30	1.993	9.388	-20.420	1.00	17.60	ATOM	204	CD	GLN	39	-0.728	29.737	-6.491	1.00	17.60
ATOM	140	O	TRP	30	3.107	9.848	-20.501	1.00	17.60	ATOM	205	OE	GLN	39	-1.061	30.597	-5.454	1.00	17.60
ATOM	141	N	GLU	31	1.056	9.587	-21.311	1.00	17.60	ATOM	206	NE	GLN	39	-1.416	29.563	-7.634	1.00	17.60
ATOM	142	CA	GLU	31	1.262	10.417	-22.651	1.00	17.60	ATOM	207	C	GLN	39	0.984	26.284	-4.331	1.00	17.60
ATOM	143	CB	GLU	31	0.404	9.918	-23.608	1.00	17.60	ATOM	208	O	GLN	39	0.054	26.148	-3.429	1.00	17.60
ATOM	144	CG	GLU	31	1.180	8.804	-24.289	1.00	17.60	ATOM	209	N	LEU	40	2.186	26.560	-4.057	1.00	17.60
ATOM	145	CD	GLU	31	0.420	7.977	-25.323	1.00	17.60	ATOM	210	CA	LEU	40	2.791	26.451	-2.705	1.00	17.60
ATOM	146	OE	GLU	31	0.071	6.535	-26.389	1.00	17.60	ATOM	211	CB	LEU	40	6.200	27.087	-2.926	1.00	17.60
ATOM	147	CE	GLU	31	0.224	6.767	-25.038	1.00	17.60	ATOM	212	CG	LEU	40	5.404	26.933	-2.007	1.00	17.60
ATOM	148	C	GLU	31	0.977	11.856	-22.225	1.00	17.60	ATOM	213	CD	LEU	40	5.689	28.318	-1.462	1.00	17.60
ATOM	149	O	GLU	31	1.617	12.709	-22.862	1.00	17.60	ATOM	214	CD	LEU	40	5.196	25.882	-0.934	1.00	17.60
ATOM	150	N	ASP	32	-0.020	12.135	-21.374	1.00	17.60	ATOM	215	C	LEU	40	2.027	26.986	-1.454	1.00	17.60
ATOM	151	CA	ASP	32	-0.380	13.519	-21.120	1.00	17.60	ATOM	216	O	LEU	40	1.587	26.281	-0.549	1.00	17.60
ATOM	152	CB	ASP	32	-1.806	13.076	-21.385	1.00	17.60	ATOM	217	N	ASP	41	1.719	28.259	-1.672	1.00	17.60
ATOM	153	CG	ASP	32	-2.383	13.211	-22.630	1.00	17.60	ATOM	218	CA	ASP	41	1.042	29.206	-0.839	1.00	17.60
ATOM	154	OD	ASP	32	-1.715	13.229	-23.685	1.00	17.60	ATOM	219	CB	ASP	41	0.821	30.436	-1.716	1.00	17.60
ATOM	155	OD	ASP	32	-3.513	12.684	-22.528	1.00	17.60	ATOM	220	CG	ASP	41	-0.499	30.564	-2.545	1.00	17.60
ATOM	156	C	ASP	32	-0.224	13.515	-19.618	1.00	17.60	ATOM	221	OD	ASP	41	-0.940	31.725	-2.738	1.00	17.60
ATOM	157	O	ASP	32	-1.090	13.026	-18.934	1.00	17.60	ATOM	222	OD	ASP	41	-3.104	29.553	-2.975	1.00	17.60
ATOM	158	N	PRO	33	0.963	13.902	-19.213	1.00	17.60	ATOM	223	C	ASP	41	-0.253	28.734	-0.247	1.00	17.60
ATOM	159	CD	PRO	33	2.250	13.686	-19.880	1.00	17.60	ATOM	224	O	ASP	41	-0.808	29.339	0.611	1.00	17.60
ATOM	160	CA	PRO	33	1.194	14.234	-17.839	1.00	17.60	ATOM	225	N	GLN	42	-0.807	27.741	-0.880	1.00	17.60
ATOM	161	CB	PRO	33	2.739	14.198	-17.767	1.00	17.60	ATOM	226	CA	GLN	42	-2.036	27.326	-0.374	1.00	17.60
ATOM	162	CG	PRO	33	3.186	14.611	-19.154	1.00	17.60	ATOM	227	CB	GLN	42	-2.919	27.329	-1.577	1.00	17.60
ATOM	163	C	PRO	33	0.521	15.528	-17.350	1.00	17.60	ATOM	228	CG	GLN	42	-2.650	25.992	-2.512	1.00	17.60
ATOM	164	O	PRO	33	0.012	16.322	-18.173	1.00	17.60	ATOM	229	CD	GLN	42	-2.883	26.370	-3.970	1.00	17.60
ATOM	165	N	SER	34	0.535	15.659	-16.013	1.00	17.60	ATOM	230	OE	GLN	42	-2.444	27.439	-4.418	1.00	17.60
ATOM	166	CA	SER	34	0.072	16.832	-15.310	1.00	17.60	ATOM	231	NE	GLN	42	-3.557	25.530	-6.782	1.00	17.60
ATOM	167	CB	SER	34	-0.516	16.425	-13.995	1.00	17.60	ATOM	232	C	GLN	42	-2.081	26.115	0.529	1.00	17.60
ATOM	168	CG	SER	34	-1.502	15.451	-14.263	1.00	17.60	ATOM	233	O	GLN	42	-3.041	25.511	0.823	1.00	17.60
ATOM	169	C	SER	34	1.224	17.806	-15.065	1.00	17.60	ATOM	234	N	PHE	43	-0.796	25.784	0.981	1.00	17.60
ATOM	170	O	SER	34	2.387	17.445	-14.841	1.00	17.60	ATOM	235	CA	PHE	43	-0.521	24.696	1.881	1.00	17.60
ATOM	171	N	GLN	35	0.863	19.075	-15.089	1.00	17.60	ATOM	236	CB	PHE	43	0.476	23.683	1.316	1.00	17.60
ATOM	172	CA	GLN	35	1.032	20.127	-14.999	1.00	17.60	ATOM	237	CG	PHE	43	-0.091	22.886	0.147	1.00	17.60
ATOM	173	CB	GLN	35	1.510	21.138	-16.155	1.00	17.60	ATOM	238	CD	PHE	43	-0.818	21.783	0.389	1.00	17.60
ATOM	174	CG	GLN	35	2.298	21.021	-17.486	1.00	17.60	ATOM	239	CD	PHE	43	0.090	23.337	-1.126	1.00	17.60
ATOM	175	CD	GLN	35	3.820	21.101	-17.327	1.00	17.60	ATOM	240	CE	PHE	43	-1.434	21.143	-0.646	1.00	17.60
ATOM	176	OE	GLN	35	6.570	20.435	-18.044	1.00	17.60	ATOM	241	CE	PHE	43	-0.508	22.676	-2.157	1.00	17.60
ATOM	177	NE	GLN	35	4.389	21.893	-16.433	1.00	17.60	ATOM	242	CE	PHE	43	-1.271	21.585	-1.922	1.00	17.60
ATOM	178	C	GLN	35	1.772	20.757	-13.592	1.00	17.60	ATOM	243	C	PHE	43	0.138	25.100	2.984	1.00	17.60
ATOM	179	O	GLN	35	2.032	20.065	-12.593	1.00	17.60	ATOM	244	O	PHE	44	1.028	26.250	2.767	1.00	17.60
ATOM	180	N	ASN	36	3.362	22.041	-13.470	1.00	17.60	ATOM	245	N	ASP	44	-0.285	25.003	4.166	1.00	17.60
ATOM	181	CA	ASN	36	1.316	22.717	-12.188	1.00	17.60	ATOM	246	CA	ASP	44	0.297	25.527	5.395	1.00	17.60
ATOM	182	CB	ASN	36	1.963	24.116	-12.270	1.00	17.60	ATOM	247	CB	ASP	44	-0.777	25.931	6.353	1.00	17.60
ATOM	183	CG	ASN	36	3.389	24.158	-11.671	1.00	17.60	ATOM	248	CG	ASP	44	-0.387	27.241	7.069	1.00	17.60
ATOM	184	OD	ASN	36	3.695	25.022	-10.844	1.00	17.60	ATOM	249	OD	ASP	44	-0.497	27.262	8.308	1.00	17.60
ATOM	185	OD	ASN	36	4.332	23.267	-12.005	1.00	17.60	ATOM	250	OD	ASP	44	0.016	28.246	6.433	1.00	17.60
ATOM	186	C	ASN	36	-0.121	22.852	-11.741	1.00	17.60	ATOM	251	C	ASP	44	1.042	24.327	5.901	1.00	17.60
ATOM	187	O	ASN	36	-0.850	23.796	-12.035	1.00	17.60	ATOM	252	O	ASP	44	0.446	23.234	5.854	1.00	17.60
ATOM	188	N	THR	37	-0.429	21.720	-11.128	1.00	17.60	ATOM	253	N	ARG	45	2.309	24.588	6.329	1.00	17.60
ATOM	189	CA	THR	37	-1.650	21.381	-10.413	1.00	17.60	ATOM	254	CA	ARG	45	3.337	23.576	6.654	1.00	17.60
ATOM	190	CB	THR	37	-1.625	19.938	-9.989	1.00	17.60	ATOM	255	CB	ARG	45	4.671	23.942	5.952	1.00	17.60
ATOM	191	CG	THR	37	-1.226	19.085	-11.071	1.00	17.60	ATOM	256	CG	ARG	45	5.807	24.822	6.586	1.00	17.60
ATOM	192	CD	THR	37	-2.993	18.553	-9.497	1.00	17.60	ATOM	257	CD	ARG	45	6.831	24.667	7.111	1.00	17.60

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ATOM	258	NE	ARG	45	0.109	24.601	7.476	1.00	17.60	ATOM	323	CE1	PHE	54	19.985	11.398	-4.683	1.00	17.60
ATOM	259	CE	ARG	45	0.709	25.370	8.477	1.00	17.60	ATOM	324	CE2	PHE	54	17.650	11.003	-4.910	1.00	17.60
ATOM	260	NH1	ARG	45	0.021	25.738	9.505	1.00	17.60	ATOM	325	C2	PHE	54	10.941	10.507	-4.827	1.00	17.60
ATOM	261	NH2	ARG	45	10.007	25.735	8.433	1.00	17.60	ATOM	326	C	PHE	54	16.767	15.469	-2.728	1.00	17.60
ATOM	262	O	ARG	45	3.703	23.196	8.089	1.00	17.60	ATOM	327	O	PHE	54	16.202	16.596	-2.728	1.00	17.60
ATOM	263	N	ILE	45	6.105	24.057	8.839	1.00	17.60	ATOM	328	N	GLY	55	16.100	14.340	-2.499	1.00	17.60
ATOM	264	CA	ILE	45	3.597	21.083	8.434	1.00	17.60	ATOM	329	CA	GLY	55	14.764	16.257	-1.950	1.00	17.60
ATOM	265	CB	ILE	45	3.794	21.479	9.789	1.00	17.60	ATOM	330	C	GLY	55	14.644	15.193	-0.761	1.00	17.60
ATOM	266	CD	ILE	46	2.021	20.312	10.090	1.00	17.60	ATOM	331	O	GLY	55	13.736	16.032	-0.631	1.00	17.60
ATOM	267	CG1	ILE	46	2.073	20.139	11.594	1.00	17.60	ATOM	332	N	ARG	56	15.627	15.015	0.099	1.00	17.60
ATOM	268	CG1	ILE	46	1.380	20.590	9.628	1.00	17.60	ATOM	333	CA	ARG	56	15.776	15.966	1.146	1.00	17.60
ATOM	269	CD1	ILE	46	0.690	21.965	9.979	1.00	17.60	ATOM	334	CB	ARG	56	16.515	17.169	0.499	1.00	17.60
ATOM	270	C	ILE	46	5.211	20.974	10.073	1.00	17.60	ATOM	335	CG	ARG	56	18.035	16.734	0.270	1.00	17.60
ATOM	271	O	ILE	46	5.906	21.775	10.597	1.00	17.60	ATOM	336	CD	ARG	56	18.907	16.107	1.434	1.00	17.60
ATOM	272	N	LYS	47	5.659	19.766	9.765	1.00	17.60	ATOM	337	NE	ARG	56	18.543	16.650	2.742	1.00	17.60
ATOM	273	CA	LYS	47	7.014	19.387	10.146	1.00	17.60	ATOM	338	CE	ARG	56	18.964	16.231	3.935	1.00	17.60
ATOM	274	CB	LYS	47	7.072	18.778	11.591	1.00	17.60	ATOM	339	NH1	ARG	56	19.004	15.207	4.065	1.00	17.60
ATOM	275	CG	LYS	47	6.566	17.394	12.064	1.00	17.60	ATOM	340	NH2	ARG	56	16.545	16.910	5.021	1.00	17.60
ATOM	276	CD	LYS	47	7.572	16.224	12.313	1.00	17.60	ATOM	341	C	ARG	56	14.515	16.347	1.886	1.00	17.60
ATOM	277	CE	LYS	47	8.029	16.390	12.339	1.00	17.60	ATOM	342	O	ARG	56	13.033	15.387	2.189	1.00	17.60
ATOM	278	N2	LYS	47	10.045	16.059	12.546	1.00	17.60	ATOM	343	N	VAL	57	14.052	17.560	2.121	1.00	17.60
ATOM	279	C	LYS	47	7.571	18.170	9.177	1.00	17.60	ATOM	344	CA	VAL	57	13.050	17.719	3.102	1.00	17.60
ATOM	280	O	LYS	47	6.837	17.729	8.425	1.00	17.60	ATOM	345	CB	VAL	57	13.014	19.327	3.504	1.00	17.60
ATOM	281	N	THR	48	0.880	18.210	9.284	1.00	17.60	ATOM	346	CG1	VAL	57	12.180	20.277	2.663	1.00	17.60
ATOM	282	CA	THR	48	9.671	17.302	8.501	1.00	17.60	ATOM	347	CG2	VAL	57	12.492	19.422	4.949	1.00	17.60
ATOM	283	CB	THR	48	11.026	17.905	8.610	1.00	17.60	ATOM	348	C	VAL	57	11.713	17.091	2.732	1.00	17.60
ATOM	284	CG1	THR	48	10.787	19.207	8.034	1.00	17.60	ATOM	349	O	VAL	57	11.620	16.901	1.534	1.00	17.60
ATOM	285	CG2	THR	48	12.352	17.122	7.984	1.00	17.60	ATOM	350	N	MET	58	10.950	16.665	3.746	1.00	17.60
ATOM	286	C	THR	48	9.554	15.860	8.940	1.00	17.60	ATOM	351	CA	MET	58	9.680	15.995	3.532	1.00	17.60
ATOM	287	O	THR	48	10.119	15.407	9.937	1.00	17.60	ATOM	352	CB	MET	58	10.129	14.616	3.336	1.00	17.60
ATOM	288	N	LEU	49	0.679	15.197	8.233	1.00	17.60	ATOM	353	CG	MET	58	9.486	14.217	2.096	1.00	17.60
ATOM	289	CA	LEU	49	6.401	13.021	8.449	1.00	17.60	ATOM	354	SD	MET	58	8.118	13.359	2.895	1.00	17.60
ATOM	290	CB	LEU	49	7.338	13.369	7.512	1.00	17.60	ATOM	355	CE	MET	58	9.092	11.853	3.020	1.00	17.60
ATOM	291	CG	LEU	49	5.952	13.869	7.766	1.00	17.60	ATOM	356	C	MET	58	8.759	16.257	4.733	1.00	17.60
ATOM	292	CD1	LEU	49	5.078	13.387	6.647	1.00	17.60	ATOM	357	O	MET	58	8.716	15.559	5.741	1.00	17.60
ATOM	293	CD2	LEU	49	5.429	13.371	9.097	1.00	17.60	ATOM	358	N	LEU	59	8.076	17.374	4.566	1.00	17.60
ATOM	294	C	LEU	49	9.620	12.981	8.216	1.00	17.60	ATOM	359	CA	LEU	59	7.269	18.051	5.512	1.00	17.60
ATOM	295	O	LEU	49	9.935	12.123	9.052	1.00	17.60	ATOM	360	CB	LEU	59	7.270	19.543	5.146	1.00	17.60
ATOM	296	N	GLY	50	10.276	12.192	7.068	1.00	17.60	ATOM	361	CD	LEU	59	8.353	20.540	4.697	1.00	17.60
ATOM	297	CA	GLY	50	11.429	12.399	6.695	1.00	17.60	ATOM	362	CD1	LEU	59	7.624	21.728	4.178	1.00	17.60
ATOM	298	C	GLY	50	12.442	13.264	5.988	1.00	17.60	ATOM	363	CD2	LEU	59	9.230	21.069	5.801	1.00	17.60
ATOM	299	O	GLY	50	12.205	14.419	5.442	1.00	17.60	ATOM	364	C	LEU	59	5.028	17.552	5.497	1.00	17.60
ATOM	300	N	THR	51	13.630	12.769	5.802	1.00	17.60	ATOM	365	O	LEU	59	5.327	17.479	4.370	1.00	17.60
ATOM	301	CA	THR	51	14.560	13.512	5.000	1.00	17.60	ATOM	366	N	VAL	60	5.054	17.225	6.552	1.00	17.60
ATOM	302	CB	THR	51	15.596	14.100	5.938	1.00	17.60	ATOM	367	CA	VAL	60	3.596	17.017	6.466	1.00	17.60
ATOM	303	CG1	THR	51	15.964	15.301	5.265	1.00	17.60	ATOM	368	CB	VAL	60	2.873	16.300	7.754	1.00	17.60
ATOM	304	CG2	THR	51	16.810	13.349	6.254	1.00	17.60	ATOM	369	CG1	VAL	60	3.013	17.069	9.050	1.00	17.60
ATOM	305	C	THR	51	15.113	12.417	4.123	1.00	17.60	ATOM	370	CG2	VAL	60	1.366	16.200	7.569	1.00	17.60
ATOM	306	O	THR	51	14.728	11.247	6.317	1.00	17.60	ATOM	371	C	VAL	60	3.044	18.408	6.375	1.00	17.60
ATOM	307	N	GLY	52	15.958	12.742	3.145	1.00	17.60	ATOM	372	O	VAL	60	3.602	19.330	6.979	1.00	17.60
ATOM	308	CA	GLY	52	16.599	11.722	2.295	1.00	17.60	ATOM	373	N	LYS	61	2.001	18.629	5.601	1.00	17.60
ATOM	309	C	GLY	52	17.729	12.371	1.492	1.00	17.60	ATOM	374	CA	LYS	61	1.271	19.886	5.690	1.00	17.60
ATOM	310	O	GLY	52	17.903	13.550	1.819	1.00	17.60	ATOM	375	CB	LYS	61	1.586	20.883	4.567	1.00	17.60
ATOM	311	N	SER	53	18.538	11.007	0.556	1.00	17.60	ATOM	376	CG	LYS	61	2.742	20.769	3.692	1.00	17.60
ATOM	312	CA	SER	53	19.369	12.712	-0.211	1.00	17.60	ATOM	377	CD	LYS	61	2.378	19.569	2.878	1.00	17.60
ATOM	313	CB	SER	53	20.556	12.112	-0.777	1.00	17.60	ATOM	378	CE	LYS	61	1.016	19.519	2.112	1.00	17.60
ATOM	314	CG	SER	53	21.209	13.380	-0.990	1.00	17.60	ATOM	379	NE	LYS	61	-0.137	19.201	2.962	1.00	17.60
ATOM	315	C	SER	53	18.599	12.211	-1.401	1.00	17.60	ATOM	380	C	LYS	61	-0.253	19.682	5.695	1.00	17.60
ATOM	316	O	SER	53	17.719	12.495	-1.808	1.00	17.60	ATOM	381	O	LYS	61	-0.782	18.584	5.959	1.00	17.60
ATOM	317	N	PHE	54	18.919	16.449	-1.964	1.00	17.60	ATOM	382	N	His	62	-0.993	20.743	5.432	1.00	17.60
ATOM	318	CA	PHE	54	18.231	15.267	-3.033	1.00	17.60	ATOM	383	CA	His	62	-2.415	20.037	5.610	1.00	17.60
ATOM	319	CB	PHE	54	18.194	16.724	-4.518	1.00	17.60	ATOM	384	CB	His	62	-2.705	21.658	6.769	1.00	17.60
ATOM	320	CO	PHE	54	18.455	13.239	-4.695	1.00	17.60	ATOM	385	CG	His	62	-4.039	21.721	7.497	1.00	17.60
ATOM	321	CD1	PHE	54	19.751	12.765	-4.618	1.00	17.60	ATOM	386	CD2	His	62	-4.267	22.732	8.413	1.00	17.60
ATOM	322	CD2	PHE	54	17.397	12.367	-4.847	1.00	17.60	ATOM	387	ND1	His	62	-5.125	20.915	7.574	1.00	17.60

ATOM	388	CE1 HIS	62	-5.957	21.386	8.522	1.00	17.60	ATOM	453	C	ALA	70	3.783	15.795	1.533	1.00	17.60
ATOM	389	NE2 HIS	62	-5.431	22.491	9.044	1.00	17.60	ATOM	454	O	ALA	70	3.437	15.320	0.450	1.00	17.60
ATOM	390	C HIS	62	-2.588	21.690	6.437	1.00	17.60	ATOM	455	N	MET	71	4.548	16.909	1.586	1.00	17.60
ATOM	391	O HIS	62	-1.861	22.678	6.233	1.00	17.60	ATOM	456	CA	MET	71	5.139	17.483	0.365	1.00	17.60
ATOM	392	N HIS	63	-3.452	21.170	3.615	1.00	17.60	ATOM	457	CB	MET	71	5.282	18.983	0.401	1.00	17.60
ATOM	393	CA LYS	63	-0.021	21.905	2.508	1.00	17.60	ATOM	458	CG	MET	71	4.212	19.775	-0.254	1.00	17.60
ATOM	394	CB LYS	63	-4.988	21.035	1.702	1.00	17.60	ATOM	459	SD	MET	71	4.873	21.446	-0.425	1.00	17.60
ATOM	395	CG LYS	63	-5.893	21.856	0.736	1.00	17.60	ATOM	460	CE	MET	71	3.859	22.475	0.586	1.00	17.60
ATOM	396	CD LYS	63	-5.748	21.202	-0.598	1.00	17.60	ATOM	461	C	MET	71	6.566	16.969	0.125	1.00	17.60
ATOM	397	CE LYS	63	-5.648	22.261	-3.616	1.00	17.60	ATOM	462	O	MET	71	7.301	16.966	1.121	1.00	17.60
ATOM	398	NE LYS	63	-4.632	22.398	-3.236	1.00	17.60	ATOM	463	N	LYS	72	7.069	16.516	-1.031	1.00	17.60
ATOM	399	C LYS	63	-4.836	22.931	3.236	1.00	17.60	ATOM	464	CA	LYS	72	8.474	16.136	-1.230	1.00	17.60
ATOM	400	O LYS	63	-5.608	22.468	4.093	1.00	17.60	ATOM	465	CB	LYS	72	8.639	14.971	-2.188	1.00	17.60
ATOM	401	N GLU	64	-4.809	24.235	2.942	1.00	17.60	ATOM	466	CG	LYS	72	9.921	14.141	-2.247	1.00	17.60
ATOM	402	CA GLU	64	-5.653	25.218	3.629	1.00	17.60	ATOM	467	CD	LYS	72	9.686	13.128	-3.350	1.00	17.60
ATOM	403	CB GLU	64	-5.235	26.666	3.137	1.00	17.60	ATOM	468	CE	LYS	72	10.693	12.015	-3.314	1.00	17.60
ATOM	404	CD GLU	64	-3.724	27.045	3.392	1.00	17.60	ATOM	469	NE	LYS	72	11.931	12.403	-3.932	1.00	17.60
ATOM	405	DE GLU	64	-3.314	28.509	3.676	1.00	17.60	ATOM	470	C	LYS	72	9.038	17.379	-1.867	1.00	17.60
ATOM	406	OE1 GLU	64	-4.039	29.162	6.418	1.00	17.60	ATOM	471	O	LYS	72	8.510	17.064	-2.872	1.00	17.60
ATOM	407	OE2 GLU	64	-2.265	29.082	3.198	1.00	17.60	ATOM	472	N	ILE	73	10.066	17.973	-1.325	1.00	17.60
ATOM	408	C GLU	64	-7.175	24.965	3.454	1.00	17.60	ATOM	473	CA	ILE	73	10.516	19.214	-1.851	1.00	17.60
ATOM	409	O GLU	64	-7.980	25.886	3.643	1.00	17.60	ATOM	474	CB	ILE	73	10.552	20.295	-0.782	1.00	17.60
ATOM	410	N SER	65	-7.664	23.768	3.079	1.00	17.60	ATOM	475	CG1 ILE	73	10.818	21.641	-1.462	1.00	17.60	
ATOM	411	CA SER	65	-9.057	23.326	3.010	1.00	17.60	ATOM	476	CG1 ILE	73	9.201	20.263	0.036	1.00	17.60	
ATOM	412	CB SER	65	-9.613	23.537	1.638	1.00	17.60	ATOM	477	CD1 ILE	73	9.227	21.445	0.988	1.00	17.60	
ATOM	413	OO SER	65	-9.657	24.945	1.394	1.00	17.60	ATOM	478	C	ILE	73	11.921	18.870	-3.232	1.00	17.60
ATOM	414	O SER	65	-9.251	21.876	3.406	1.00	17.60	ATOM	479	O	ILE	73	12.721	16.747	-1.293	1.00	17.60
ATOM	415	C SER	65	-9.735	20.999	2.697	1.00	17.60	ATOM	480	N	LEU	74	12.139	18.696	-3.561	1.00	17.60
ATOM	416	N GLY	66	-9.724	21.668	4.599	1.00	17.60	ATOM	481	CA	LEU	74	13.427	18.498	-4.269	1.00	17.60
ATOM	417	CA GLY	66	-9.009	20.469	5.313	1.00	17.60	ATOM	482	CB	LEU	74	13.316	17.822	-5.623	1.00	17.60
ATOM	418	C GLY	66	-7.841	19.560	5.575	1.00	17.60	ATOM	483	CG	LEU	74	13.044	16.409	-5.884	1.00	17.60
ATOM	419	O GLY	66	-7.288	19.560	6.670	1.00	17.60	ATOM	484	CD1 LEU	74	14.154	15.122	-5.168	1.00	17.60	
ATOM	420	N ASN	67	-2.443	18.993	4.465	1.00	17.60	ATOM	485	CD2 LEU	74	11.732	15.967	-5.291	1.00	17.60	
ATOM	421	CA ASN	67	-6.574	17.861	4.513	1.00	17.60	ATOM	486	C	LEU	74	14.024	19.854	-4.616	1.00	17.60
ATOM	422	CB ASN	67	-6.631	17.021	3.255	1.00	17.60	ATOM	487	O	LEU	74	13.371	20.722	-5.203	1.00	17.60
ATOM	423	CG ASN	67	-8.024	16.603	2.884	1.00	17.60	ATOM	488	N	ASP	75	15.294	20.063	-4.358	1.00	17.60
ATOM	424	OD1 ASN	67	-8.514	15.599	3.340	1.00	17.60	ATOM	489	CA	ASP	75	15.864	21.384	-4.577	1.00	17.60
ATOM	425	ND2 ASN	67	-8.612	17.407	2.022	1.00	17.60	ATOM	490	CB	ASP	75	17.023	21.597	-4.577	1.00	17.60
ATOM	426	C ASN	67	-5.102	17.987	4.757	1.00	17.60	ATOM	491	CG	ASP	75	17.047	22.892	-3.561	1.00	17.60
ATOM	427	O ASN	67	-4.534	19.068	4.657	1.00	17.60	ATOM	492	OD1 ASP	75	18.303	23.194	-4.748	1.00	17.60	
ATOM	428	N HIS	68	-4.525	16.841	5.115	1.00	17.60	ATOM	493	OD2 ASP	75	18.016	23.592	-2.647	1.00	17.60	
ATOM	429	CA HIS	68	-3.105	16.720	5.349	1.00	17.60	ATOM	494	C	ASP	75	16.349	21.356	-5.996	1.00	17.60
ATOM	430	CB HIS	68	-2.853	16.115	6.720	1.00	17.60	ATOM	495	O	ASP	75	17.334	20.626	-6.189	1.00	17.60
ATOM	431	CG HIS	68	-3.156	17.072	7.865	1.00	17.60	ATOM	496	N	LYS	76	15.812	22.105	-6.962	1.00	17.60
ATOM	432	CD2 HIS	68	-4.291	17.052	8.606	1.00	17.60	ATOM	497	CA	LYS	76	16.296	21.980	-8.366	1.00	17.60
ATOM	433	ND1 HIS	68	-2.371	18.021	9.350	1.00	17.60	ATOM	498	CB	LYS	76	15.825	23.151	-9.221	1.00	17.60
ATOM	434	CE1 HIS	68	-2.962	18.580	9.353	1.00	17.60	ATOM	499	CG	LYS	76	16.393	22.951	-9.711	1.00	17.60
ATOM	435	NE2 HIS	68	-6.106	17.987	9.486	1.00	17.60	ATOM	500	CD	LYS	76	13.857	23.988	-10.680	1.00	17.60
ATOM	436	C HIS	68	-2.569	15.824	4.236	1.00	17.60	ATOM	501	CE	LYS	76	16.099	25.407	-10.127	1.00	17.60
ATOM	437	O HIS	68	-3.278	15.041	3.615	1.00	17.60	ATOM	502	NE	LYS	76	13.055	26.340	-10.483	1.00	17.60
ATOM	438	N TYR	69	-1.265	15.957	3.983	1.00	17.60	ATOM	503	C	LYS	76	17.070	21.864	-8.522	1.00	17.60
ATOM	439	CA TYR	69	-0.622	15.375	2.843	1.00	17.60	ATOM	504	O	LYS	76	18.241	20.886	-9.139	1.00	17.60
ATOM	440	CB TYR	69	-0.865	16.235	1.563	1.00	17.60	ATOM	505	N	GLN	77	18.665	22.716	-7.856	1.00	17.60
ATOM	441	CG TYR	69	-2.254	16.372	0.908	1.00	17.60	ATOM	506	CA	GLN	77	20.154	22.762	-7.969	1.00	17.60
ATOM	442	CD1 TYR	69	-3.013	15.273	0.628	1.00	17.60	ATOM	507	CB	GLN	77	20.883	23.889	-7.273	1.	

ATOM	518	CD	LVS	78	19.876	19.183	-1.976	1.00	17.60	16.043	10.985	-17.407	1.00	17.60
ATOM	519	CE	LVS	78	20.979	10.496	-1.095	1.00	17.60	15.076	11.726	-18.374	1.00	17.60
ATOM	520	N2	LVS	78	21.013	17.000	-3.167	1.00	17.60	13.051	11.404	-18.384	1.00	17.60
ATOM	521	C	LVS	78	20.860	16.726	-6.414	1.00	17.60	13.560	12.552	-19.136	1.00	17.60
ATOM	522	O	LVS	78	21.716	17.034	-6.553	1.00	17.60	13.537	11.847	-16.413	1.00	17.60
ATOM	523	N	VAL	79	19.663	18.696	-7.063	1.00	17.60	14.280	11.703	-14.597	1.00	17.60
ATOM	524	CA	VAL	79	19.252	17.606	-7.975	1.00	17.60	16.035	11.259	-13.338	1.00	17.60
ATOM	525	CR	VAL	79	17.707	17.750	-8.319	1.00	17.60	15.113	10.446	-12.532	1.00	17.60
ATOM	526	CG1	VAL	78	17.391	17.194	-9.668	1.00	17.60	15.727	9.448	-11.537	1.00	17.60
ATOM	527	CG2	VAL	79	16.040	16.770	-7.535	1.00	17.60	17.003	8.641	-11.058	1.00	17.60
ATOM	528	C	VAL	79	20.114	17.607	-9.266	1.00	17.60	18.119	8.826	-11.108	1.00	17.60
ATOM	529	O	VAL	79	20.471	16.533	-9.797	1.00	17.60	17.327	7.679	-12.711	1.00	17.60
ATOM	530	N	VAL	80	20.485	18.791	-9.702	1.00	17.60	18.551	7.308	-12.496	1.00	17.60
ATOM	531	CA	VAL	80	21.324	18.929	-10.965	1.00	17.60	19.012	8.005	-11.528	1.00	17.60
ATOM	532	CB	VAL	80	21.236	20.402	-11.533	1.00	17.60	14.352	11.361	-11.680	1.00	17.60
ATOM	533	CG1	VAL	80	22.059	20.499	-12.782	1.00	17.60	13.380	10.833	-11.038	1.00	17.60
ATOM	534	CG2	VAL	80	19.030	20.793	-11.975	1.00	17.60	14.357	12.674	-11.617	1.00	17.60
ATOM	535	C	VAL	80	22.736	18.571	-10.523	1.00	17.60	13.349	13.498	-10.934	1.00	17.60
ATOM	536	O	VAL	80	23.000	17.913	-11.246	1.00	17.60	13.979	14.911	-10.816	1.00	17.60
ATOM	537	K	LVS	81	23.104	18.099	-9.292	1.00	17.60	14.995	14.096	-9.818	1.00	17.60
ATOM	538	CA	LVS	81	26.419	18.569	-8.795	1.00	17.60	12.968	15.930	-10.465	1.00	17.60
ATOM	539	CB	LVS	81	24.585	18.969	-7.382	1.00	17.60	12.065	13.494	-11.837	1.00	17.60
ATOM	540	CG	LVS	81	25.391	20.214	-7.164	1.00	17.60	10.895	13.407	-11.455	1.00	17.60
ATOM	541	CD	LVS	81	24.710	21.443	-7.699	1.00	17.60	12.306	13.487	-13.118	1.00	17.60
ATOM	542	CE	LVS	81	25.375	22.618	-7.033	1.00	17.60	11.311	13.632	-14.152	1.00	17.60
ATOM	543	N2	LVS	81	25.193	22.570	-9.601	1.00	17.60	12.123	14.039	-15.377	1.00	17.60
ATOM	544	C	LVS	81	24.702	17.095	-8.823	1.00	17.60	12.826	15.444	-15.260	1.00	17.60
ATOM	545	O	LVS	81	25.718	16.641	-9.330	1.00	17.60	13.069	15.545	-16.328	1.00	17.60
ATOM	546	N	LEU	82	23.733	16.391	-8.226	1.00	17.60	11.816	16.591	-15.333	1.00	17.60
ATOM	547	CA	LEU	82	23.799	14.971	-7.988	1.00	17.60	10.402	12.615	-14.309	1.00	17.60
ATOM	548	CB	LEU	82	22.905	14.670	-6.779	1.00	17.60	9.275	12.529	-14.389	1.00	17.60
ATOM	549	CG	LEU	82	23.361	14.917	-5.312	1.00	17.60	11.141	11.270	-14.212	1.00	17.60
ATOM	550	CD1	LEU	82	24.485	15.939	-5.147	1.00	17.60	10.507	9.954	-14.227	1.00	17.60
ATOM	551	CD2	LEU	82	22.179	15.530	-6.583	1.00	17.60	11.395	8.734	-14.201	1.00	17.60
ATOM	552	C	LEU	82	23.450	14.132	-9.200	1.00	17.60	12.357	8.498	-15.338	1.00	17.60
ATOM	553	O	LEU	82	23.467	12.908	-9.132	1.00	17.60	12.012	8.535	-16.514	1.00	17.60
ATOM	554	N	LVS	83	23.254	14.767	-10.373	1.00	17.60	13.613	8.175	-15.045	1.00	17.60
ATOM	555	CA	LVS	83	23.034	14.042	-11.657	1.00	17.60	9.771	9.713	-12.976	1.00	17.60
ATOM	556	CB	LVS	83	24.152	12.947	-11.886	1.00	17.60	8.758	8.938	-13.018	1.00	17.60
ATOM	557	CG	LVS	83	25.634	13.37	-11.937	1.00	17.60	10.058	10.294	-11.819	1.00	17.60
ATOM	558	CD	LVS	83	26.578	12.06	-12.059	1.00	17.60	9.221	10.000	-10.673	1.00	17.60
ATOM	559	CE	LVS	83	28.302	12.495	-12.088	1.00	17.60	9.911	10.261	-9.359	1.00	17.60
ATOM	560	N2	LVS	83	29.018	13.417	-12.425	1.00	17.60	10.200	11.651	-8.819	1.00	17.60
ATOM	561	C	LVS	83	21.666	13.372	-11.713	1.00	17.60	10.923	11.556	-7.524	1.00	17.60
ATOM	562	O	LVS	83	21.434	12.382	-12.454	1.00	17.60	10.343	10.981	-6.599	1.00	17.60
ATOM	563	N	GLN	84	20.667	13.902	-10.968	1.00	17.60	12.051	12.056	-7.444	1.00	17.60
ATOM	564	CA	GLN	84	19.411	13.182	-10.969	1.00	17.60	7.919	10.767	-10.643	1.00	17.60
ATOM	565	CB	GLN	84	19.057	12.853	-9.552	1.00	17.60	6.875	10.199	-10.290	1.00	17.60
ATOM	566	CG	GLN	84	20.376	12.285	-8.669	1.00	17.60	7.932	12.066	-11.035	1.00	17.60
ATOM	567	CD	GLN	84	20.643	10.889	-9.024	1.00	17.60	6.681	12.753	-11.143	1.00	17.60
ATOM	568	CE1	GLN	84	19.874	9.960	-9.303	1.00	17.60	6.950	16.192	-11.402	1.00	17.60
ATOM	569	CE2	GLN	84	21.937	10.672	-9.091	1.00	17.60	5.691	16.995	-11.282	1.00	17.60
ATOM	570	C	GLN	84	18.278	13.934	-11.632	1.00	17.60	4.914	15.064	-12.603	1.00	17.60
ATOM	571	O	GLN	84	17.109	13.778	-11.279	1.00	17.60	5.262	16.238	-13.569	1.00	17.60
ATOM	572	N	ILE	85	18.600	14.687	-12.697	1.00	17.60	4.611	16.062	-14.839	1.00	17.60
ATOM	573	CA	ILE	85	17.540	15.538	-13.386	1.00	17.60	5.929	12.119	-12.296	1.00	17.60
ATOM	574	CB	ILE	85	18.270	16.451	-14.485	1.00	17.60	4.761	11.807	-12.089	1.00	17.60
ATOM	575	CG1	ILE	85	17.366	17.670	-14.615	1.00	17.60	6.462	11.860	-13.493	1.00	17.60
ATOM	576	CG2	ILE	85	19.632	17.002	-14.126	1.00	17.60	5.668	11.749	-14.566	1.00	17.60
ATOM	577	CD1	ILE	85	20.096	18.302	-14.805	1.00	17.60	6.568	11.160	-15.753	1.00	17.60
ATOM	578	C	ILE	85	16.699	18.560	-14.036	1.00	17.60	5.076	11.035	-17.112	1.00	17.60
ATOM	579	O	ILE	85	15.520	16.563	-13.681	1.00	17.60	6.844	11.306	-18.281	1.00	17.60
ATOM	580	N	GLU	86	17.201	13.605	-14.034	1.00	17.60	6.085	11.232	-19.523	1.00	17.60
ATOM	581	CA	GLU	86	16.276	12.693	-15.466	1.00	17.60	6.594	10.762	-20.661	1.00	17.60
ATOM	582	CB	GLU	86	17.007	11.795	-16.474	1.00	17.60	7.854	10.116	-21.111	1.00	17.60

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ATOM	648	NH2	ARG	93	5.798	10.722	-21.726	1.00	17.60	ATOM	713	O	PRO	101	-3.173	0.442	-1.542	1.00	17.60
ATOM	649	C	ARG	93	5.023	9.886	-14.274	1.00	17.60	ATOM	714	N	PHE	102	-1.649	-0.293	-3.038	1.00	17.60
ATOM	650	O	ARG	93	3.834	9.591	-14.540	1.00	17.60	ATOM	715	CA	PHE	102	-0.506	-0.267	-2.125	1.00	17.60
ATOM	651	N	ILE	94	5.830	9.043	-13.661	1.00	17.60	ATOM	716	CB	PHE	102	0.054	-1.735	-1.957	1.00	17.60
ATOM	652	CA	ILE	94	5.297	7.759	-13.306	1.00	17.60	ATOM	717	CG	PHE	102	-0.930	-2.916	-1.742	1.00	17.60
ATOM	653	CB	ILE	94	6.456	6.789	-12.958	1.00	17.60	ATOM	718	CD1	PHE	102	-0.887	-4.019	-2.603	1.00	17.60
ATOM	654	CG2	ILE	94	5.885	5.467	-12.409	1.00	17.60	ATOM	719	CD2	PHE	102	-1.883	-7.933	-0.712	1.00	17.60
ATOM	655	CG1	ILE	94	7.323	6.569	-14.191	1.00	17.60	ATOM	720	CE1	PHE	107	-1.748	-5.095	-2.462	1.00	17.60
ATOM	656	CH1	ILE	94	8.580	5.756	-33.815	1.00	17.60	ATOM	721	CE2	PHE	107	-2.742	-4.022	-0.576	1.00	17.60
ATOM	657	C	ILE	94	4.368	7.963	-32.117	1.00	17.60	ATOM	722	CA	PHE	102	-2.672	-5.092	-1.453	1.00	17.60
ATOM	658	O	ILE	94	3.251	7.448	-32.183	1.00	17.60	ATOM	723	C	PHE	102	0.543	0.693	-2.742	1.00	17.60
ATOM	659	N	LEU	95	4.605	8.709	-11.052	1.00	17.60	ATOM	724	O	PHE	102	1.742	0.472	-2.577	1.00	17.60
ATOM	660	CA	LEU	95	3.739	8.785	-9.957	1.00	17.60	ATOM	725	N	LEU	103	0.247	1.750	-3.509	1.00	17.60
ATOM	661	CB	LEU	95	4.372	9.502	-8.745	1.00	17.60	ATOM	726	CA	LEU	103	1.263	2.698	-3.944	1.00	17.60
ATOM	662	CG	LEU	95	5.054	8.546	-7.735	1.00	17.60	ATOM	727	CB	LEU	103	1.315	2.916	-5.357	1.00	17.60
ATOM	663	CD1	LEU	95	9.454	9.364	-6.612	1.00	17.60	ATOM	728	CG	LEU	103	1.974	1.983	-6.197	1.00	17.60
ATOM	664	CD2	LEU	95	4.080	7.682	-6.922	1.00	17.60	ATOM	729	CD1	LEU	103	1.312	0.638	-6.145	1.00	17.60
ATOM	665	C	LEU	95	2.405	9.443	-10.333	1.00	17.60	ATOM	730	CD2	LEU	103	1.832	2.566	-1.571	1.00	17.60
ATOM	666	O	LEU	95	1.377	9.036	-9.792	1.00	17.60	ATOM	731	C	LEU	103	0.808	4.024	-3.418	1.00	17.60
ATOM	667	N	GLN	96	2.282	10.384	-11.261	1.00	17.60	ATOM	732	O	LEU	103	-0.401	4.127	-3.231	1.00	17.60
ATOM	668	CA	GLN	96	0.971	10.898	-11.565	1.00	17.60	ATOM	733	N	VAL	104	1.574	5.080	-3.196	1.00	17.60
ATOM	669	CB	GLN	96	1.064	12.220	-12.306	1.00	17.60	ATOM	734	CA	VAL	104	0.967	6.234	-2.575	1.00	17.60
ATOM	670	CG	GLN	96	1.996	12.334	-13.505	1.00	17.60	ATOM	735	CB	VAL	104	1.834	6.750	-1.428	1.00	17.60
ATOM	671	CD	GLN	96	1.285	12.173	-14.649	1.00	17.60	ATOM	736	CG1	VAL	104	3.194	7.227	-1.906	1.00	17.60
ATOM	672	CE1	GLN	96	0.470	12.994	-15.297	1.00	17.60	ATOM	737	CG2	VAL	104	1.010	7.855	-0.716	1.00	17.60
ATOM	673	NE2	GLN	96	1.586	11.137	-15.571	1.00	17.60	ATOM	738	C	VAL	104	0.786	7.282	-3.610	1.00	17.60
ATOM	674	C	GLN	96	0.266	9.882	-12.401	1.00	17.60	ATOM	739	O	VAL	104	1.716	7.596	-4.357	1.00	17.60
ATOM	675	O	GLN	96	-0.945	9.794	-12.303	1.00	17.60	ATOM	740	N	LYS	105	-0.449	7.603	-3.568	1.00	17.60
ATOM	676	N	ALA	97	0.944	9.068	-13.208	1.00	17.60	ATOM	741	CA	LYS	105	-0.979	8.736	-4.569	1.00	17.60
ATOM	677	CA	ALA	97	0.236	8.133	-14.059	1.00	17.60	ATOM	742	CB	LYS	105	-2.470	8.934	-4.328	1.00	17.60
ATOM	678	CB	ALA	97	1.1320	7.900	-15.219	1.00	17.60	ATOM	743	CG	LYS	105	-3.467	7.803	-4.596	1.00	17.60
ATOM	679	C	ALA	97	-0.167	6.797	-13.434	1.00	17.60	ATOM	744	CD	LYS	105	-4.642	7.737	-3.554	1.00	17.60
ATOM	680	O	ALA	97	-1.067	6.098	-13.091	1.00	17.60	ATOM	745	CE	LYS	105	-4.355	6.777	-2.332	1.00	17.60
ATOM	681	N	VAL	98	0.532	6.343	-12.413	1.00	17.60	ATOM	746	N2	LYS	105	-4.578	5.335	-2.573	1.00	17.60
ATOM	682	CA	VAL	98	0.224	5.084	-11.792	1.00	17.60	ATOM	747	C	LYS	105	-0.301	10.093	-4.564	1.00	17.60
ATOM	683	CR	VAL	98	1.567	4.775	-11.104	1.00	17.60	ATOM	748	O	LYS	105	-0.028	10.626	-3.509	1.00	17.60
ATOM	684	CO1	VAL	98	1.770	5.565	-9.913	1.00	17.60	ATOM	749	N	LEU	106	-0.015	10.700	-5.701	1.00	17.60
ATOM	685	CO2	VAL	98	1.543	3.320	-10.879	1.00	17.60	ATOM	750	CA	LEU	106	0.380	11.991	-5.866	1.00	17.60
ATOM	686	C	VAL	98	-1.052	3.338	-10.888	1.00	17.60	ATOM	751	CB	LEU	106	1.469	12.029	-7.115	1.00	17.60
ATOM	687	O	VAL	98	-1.586	6.199	-10.521	1.00	17.60	ATOM	752	CG	LEU	106	2.062	13.324	-7.608	1.00	17.60
ATOM	688	N	ASN	99	-1.825	3.977	-10.516	1.00	17.60	ATOM	753	CD1	LEU	106	2.821	13.915	-6.500	1.00	17.60
ATOM	689	CA	ASN	99	-2.740	3.837	-9.555	1.00	17.60	ATOM	754	CD2	LEU	106	3.015	13.324	-8.738	1.00	17.60
ATOM	690	CB	ASN	99	-4.052	4.387	-10.136	1.00	17.60	ATOM	755	C	LEU	106	-0.674	12.716	-6.115	1.00	17.60
ATOM	691	CG	ASN	99	-3.295	4.391	-9.222	1.00	17.60	ATOM	756	O	LEU	106	-1.284	12.451	-7.124	1.00	17.60
ATOM	692	OD1	ASN	99	-6.191	5.235	-9.398	1.00	17.60	ATOM	757	N	GLU	107	-2.131	13.585	-5.196	1.00	17.60
ATOM	693	ND2	ASN	99	-5.583	3.508	-8.264	1.00	17.60	ATOM	758	CA	GLU	107	-2.315	14.385	-5.404	1.00	17.60
ATOM	694	C	ASN	99	-2.924	2.143	-9.287	1.00	17.60	ATOM	759	CB	GLU	107	-3.055	14.665	-4.107	1.00	17.60
ATOM	695	O	ASN	99	-3.281	1.531	-10.063	1.00	17.60	ATOM	760	CG	GLU	107	-4.575	14.347	-4.166	1.00	17.60
ATOM	696	N	PHE	100	-2.679	1.959	-7.941	1.00	17.60	ATOM	761	CD	GLU	107	-4.918	13.097	-3.311	1.00	17.60
ATOM	697	CA	PHE	100	-2.796	0.599	-7.442	1.00	17.60	ATOM	762	OE1	GLU	107	-4.594	13.105	-2.110	1.00	17.60
ATOM	698	CB	PHE	100	-1.481	-0.145	-7.771	1.00	17.60	ATOM	763	OE2	GLU	107	-5.485	12.318	-3.061	1.00	17.60
ATOM	699	CG	PHE	100	-1.617	-1.662	-7.671	1.00	17.60	ATOM	764	C	GLU	107	-2.032	15.721	-6.031	1.00	17.60
ATOM	700	CD1	PHE	100	-2.400	-2.350	-8.582	1.00	17.60	ATOM	765	O	GLU	107	-2.974	16.285	-6.561	1.00	17.60
ATOM	701	CD2	PHE	100	-1.075	-2.337	-6.622	1.00	17.60	ATOM	766	N	PHE	108	-0.861	16.330	-5.911	1.00	17.60
ATOM	702	CE1	PHE	100	-2.665	-3.687	-8.458	1.00	17.60	ATOM	767	CA	PHE	108	-0.535	17.542	-6.663	1.00	17.60
ATOM	703	CE2	PHE	100	-1.346	-3.687	-6.459	1.00	17.60	ATOM	768	CB	PHE	108	-0.806	18.845	-5.976	1.00	17.60
ATOM	704	CE	PHE	100	-2.133	-4.361	-7.403	1.00	17.60	ATOM	769	CG	PHE	108	-2.106	18.954	-5.139	1.00	17.60
ATOM	705	C	PHE	100	-3.038	0.719	-5.909	1.00	17.60	ATOM	770	CD1	PHE	108	-3.253	19.454	-5.737	1.00	17.60
ATOM	706	O	PHE	100	-2.635	1.746	-5.348	1.00	17.60	ATOM	771	CD2	PHE	108	-2.153	18.516	-3.831	1.00	17.60
ATOM	707	N	PRO	101	-3.657	-0.211	-5.139	1.00	17.60	ATOM	772	CE1	PHE	108	-4.452	19.506	-5.030	1.00	17.60
ATOM	708	CD	PRO	101	-4.307	-1.418	-5.637	1.00	17.60	ATOM	773	CE2	PHE	108	-3.343	18.571	-3.130	1.00	17.60
ATOM	709	CA	PRO	101	-3.995	-0.887	-3.716	1.00	17.60	ATOM	774	CE	PHE	108	-4.500	19.058	-3.715	1.00	17.60
ATOM	710	CF	PRO	101	-4.813	-1.312	-3.411	1.00	17.60	ATOM	775	C	PHE	108	0.961	17.592	-7.003	1.00	17.60
ATOM	711	CG	PRO	101	-5.468	-1.633	-4.722	1.00	17.60	ATOM	776	O	PHE	108	1.819	17.092	-6.772	1.00	17.60
ATOM	712	C	PRO	101	-2.890	0.060	-2.677	1.00	17.60	ATOM	777	N	SER	109	1.297	18.190	-8.129	1.00	17.60

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ATOM	778	CA	SER	109	2.655	10.365	-0.509	1.00	17.60	ATOM	863	CB	TYR	117	6.304	20.812	-4.462	1.00	17.60
ATOM	779	CB	SER	109	2.802	17.597	-5.065	1.00	17.60	ATOM	864	CG	TYR	117	7.033	27.102	-4.125	1.00	17.60
ATOM	780	OS	SER	109	4.217	17.409	-10.103	1.00	17.60	ATOM	865	CD1	TYR	117	7.223	27.393	-2.802	1.00	17.60
ATOM	781	C	SER	109	2.706	19.857	-0.855	1.00	17.60	ATOM	866	CE1	TYR	117	7.946	23.503	-2.440	1.00	17.60
ATOM	782	O	SER	109	1.634	20.476	-0.994	1.00	17.60	ATOM	867	CD2	TYR	117	7.549	22.933	-5.106	1.00	17.60
ATOM	783	N	PHE	110	3.076	20.486	-0.827	1.00	17.60	ATOM	868	CE2	TYR	117	0.270	24.046	-4.750	1.00	17.60
ATOM	784	CA	PHE	110	6.055	21.009	-9.142	1.00	17.60	ATOM	869	CA	TYR	117	0.401	24.335	-3.409	1.00	17.60
ATOM	785	CB	PHE	110	3.241	22.837	-0.207	1.00	17.60	ATOM	870	OH	TYR	117	9.204	25.417	-3.010	1.00	17.60
ATOM	786	CG	PHE	110	9.348	22.060	-6.779	1.00	17.60	ATOM	871	C	TYR	117	6.281	10.602	-5.630	1.00	17.60
ATOM	787	CD1	PHE	110	2.493	22.060	-6.009	1.00	17.60	ATOM	872	D	TYR	117	5.077	10.601	-6.020	1.00	17.60
ATOM	788	CD2	PHE	110	6.101	23.712	-6.135	1.00	17.60	ATOM	873	N	PHE	118	5.943	17.664	-4.771	1.00	17.60
ATOM	789	CE1	PHE	110	2.435	22.149	-4.613	1.00	17.60	ATOM	874	CA	PHE	118	4.987	16.609	-5.121	1.00	17.60
ATOM	790	CE2	PHE	110	4.116	23.792	-4.750	1.00	17.60	ATOM	875	CB	PHE	118	5.721	15.356	-5.428	1.00	17.60
ATOM	791	CZ	PHE	110	3.253	23.029	-3.970	1.00	17.60	ATOM	876	CG	PHE	118	6.485	15.405	-6.683	1.00	17.60
ATOM	792	C	PHE	110	5.408	22.211	-0.891	1.00	17.60	ATOM	877	SD	PHE	118	7.404	13.075	-6.665	1.00	17.60
ATOM	793	O	PHE	110	6.172	21.324	-0.370	1.00	17.60	ATOM	878	CB	PHE	118	8.614	14.507	-7.767	1.00	17.60
ATOM	794	N	LYS	111	5.974	23.420	-9.222	1.00	17.60	ATOM	879	C	PHE	118	4.069	16.390	-3.929	1.00	17.60
ATOM	795	CA	LYS	111	7.350	23.060	-0.922	1.00	17.60	ATOM	880	O	PHE	118	6.621	16.216	-2.862	1.00	17.60
ATOM	796	CB	LYS	111	0.306	23.391	-10.037	1.00	17.60	ATOM	881	N	VAL	119	2.755	16.344	-3.930	1.00	17.60
ATOM	797	CG	LYS	111	0.101	24.042	-11.419	1.00	17.60	ATOM	882	CA	VAL	119	2.041	16.310	-2.692	1.00	17.60
ATOM	798	CD	LYS	111	0.761	23.448	-12.679	1.00	17.60	ATOM	883	CR	VAL	119	1.091	17.472	-2.662	1.00	17.60
ATOM	799	CE	LYS	111	7.091	23.070	-13.002	1.00	17.60	ATOM	884	CG1	VAL	119	0.564	17.509	-3.263	1.00	17.60
ATOM	800	NE	LYS	111	0.166	23.370	-15.160	1.00	17.60	ATOM	885	CO2	VAL	119	1.740	10.803	-2.975	1.00	17.60
ATOM	801	C	LYS	111	7.402	25.368	-0.767	1.00	17.60	ATOM	886	C	VAL	119	1.319	15.004	-2.667	1.00	17.60
ATOM	802	O	LYS	111	6.494	26.066	-9.092	1.00	17.60	ATOM	887	O	VAL	119	0.445	14.820	-3.406	1.00	17.60
ATOM	803	N	ASP	112	0.606	25.917	-0.254	1.00	17.60	ATOM	888	N	PHE	120	1.616	14.075	-1.110	1.00	17.60
ATOM	804	CA	ASP	112	0.701	27.399	-0.214	1.00	17.60	ATOM	889	CA	PHE	120	1.057	12.730	-1.700	1.00	17.60
ATOM	805	CB	ASP	112	0.456	28.021	-6.866	1.00	17.60	ATOM	890	CB	PHE	120	2.007	11.650	-1.304	1.00	17.60
ATOM	806	CG	ASP	112	9.276	27.751	-5.627	1.00	17.60	ATOM	891	CG	PHE	120	2.961	10.910	-2.339	1.00	17.60
ATOM	807	OD1	ASP	112	10.493	27.020	-5.630	1.00	17.60	ATOM	892	SD	PHE	120	4.290	11.751	-3.236	1.00	17.60
ATOM	808	OD2	ASP	112	0.664	27.516	-4.590	1.00	17.60	ATOM	893	CE	PHE	120	5.446	11.701	-2.077	1.00	17.60
ATOM	809	C	ASP	112	10.109	27.757	-0.530	1.00	17.60	ATOM	894	C	PHE	120	0.037	12.656	-0.627	1.00	17.60
ATOM	810	O	ASP	112	10.904	26.890	-0.823	1.00	17.60	ATOM	895	O	PHE	120	0.024	13.337	0.710	1.00	17.60
ATOM	811	N	ASN	113	10.677	20.959	-0.375	1.00	17.60	ATOM	896	N	GLU	121	-0.036	11.463	-0.562	1.00	17.60
ATOM	812	CA	ASN	113	12.046	29.301	-0.770	1.00	17.60	ATOM	897	CA	GLU	121	-1.762	11.401	0.547	1.00	17.60
ATOM	813	CB	ASN	113	12.270	30.760	-0.519	1.00	17.60	ATOM	898	CB	GLU	121	-2.622	10.132	0.175	1.00	17.60
ATOM	814	CG	ASN	113	11.635	31.717	-9.547	1.00	17.60	ATOM	899	CG	GLU	121	-4.029	9.011	0.752	1.00	17.60
ATOM	815	OD1	ASN	113	10.703	32.567	-9.262	1.00	17.60	ATOM	900	CD	GLU	121	-5.010	11.000	0.925	1.00	17.60
ATOM	816	ND2	ASN	113	12.017	31.600	-10.004	1.00	17.60	ATOM	901	OE1	GLU	121	-5.961	11.170	0.107	1.00	17.60
ATOM	817	C	ASN	113	13.207	28.566	-0.199	1.00	17.60	ATOM	902	CB	GLU	121	-4.002	11.701	1.904	1.00	17.60
ATOM	818	O	ASN	113	14.205	28.630	-0.762	1.00	17.60	ATOM	903	O	GLU	121	-0.031	11.103	1.702	1.00	17.60
ATOM	819	N	SER	114	12.907	21.793	-7.144	1.00	17.60	ATOM	904	N	TYR	122	0.339	10.775	1.615	1.00	17.60
ATOM	820	CA	SER	114	16.033	27.026	-6.520	1.00	17.60	ATOM	905	CA	TYR	122	-1.229	11.496	3.036	1.00	17.60
ATOM	821	CB	SER	114	14.305	27.902	-5.162	1.00	17.60	ATOM	906	CB	TYR	122	-0.302	11.200	4.215	1.00	17.60
ATOM	822	CG	SER	114	14.610	20.964	-5.121	1.00	17.60	ATOM	907	CG	TYR	122	-0.517	12.350	5.297	1.00	17.60
ATOM	823	C	SER	114	13.714	25.544	-6.335	1.00	17.60	ATOM	908	CD1	TYR	122	-0.007	12.236	6.122	1.00	17.60
ATOM	824	O	SER	114	14.637	24.734	-6.290	1.00	17.60	ATOM	909	CE1	TYR	122	1.336	12.114	7.020	1.00	17.60
ATOM	825	N	ASN	115	12.445	25.105	-6.326	1.00	17.60	ATOM	910	CE2	TYR	122	1.763	11.920	0.337	1.00	17.60
ATOM	826	CA	ASN	115	12.119	23.703	-5.907	1.00	17.60	ATOM	911	CD2	TYR	122	-0.914	12.189	7.756	1.00	17.60
ATOM	827	CB	ASN	115	11.601	23.749	-6.409	1.00	17.60	ATOM	912	CE2	TYR	122	-0.515	12.010	9.069	1.00	17.60
ATOM	828	CG	ASN	115	12.634	24.313	-3.358	1.00	17.60	ATOM	913	CZ	TYR	122	0.073	11.001	9.354	1.00	17.60
ATOM	829	CD1	ASN	115	13.154	23.553	-2.725	1.00	17.60	ATOM	914	OX	TYR	122	1.395	11.740	10.677	1.00	17.60
ATOM	830	ND2	ASN	115	12.350	25.590	-2.995	1.00	17.60	ATOM	915	C	TYR	122	-0.782	9.025	4.773	1.00	17.60
ATOM	831	C	ASN	115	11.050	23.126	-6.749	1.00	17.60	ATOM	916	O	TYR	122	-1.937	9.490	5.034	1.00	17.60
ATOM	832	O	ASN	115	10.279	23.764	-7.449	1.00	17.60	ATOM	917	N	VAL	123	0.223	0.961	4.912	1.00	17.60
ATOM	833	N	LEU	116	10.946	21.050	-6.401	1.00	17.60	ATOM	918	CA	VAL	123	0.075	7.622	5.490	1.00	17.60
ATOM	834	CA	LEU	116	10.060	20.927	-7.120	1.00	17.60	ATOM	919	CB	VAL	123	0.071	6.550	4.595	1.00	17.60
ATOM	835	CB	LEU	116	10.069	19.900	-7.886	1.00	17.60	ATOM	920	CG1	VAL	123	0.530	5.130	5.040	1.00	17.60
ATOM	836	CG	LEU	116	11.936	20.415	-8.014	1.00	17.60	ATOM	921	CG2	VAL	123	0.424	6.540	3.140	1.00	17.60
ATOM	837	CD1	LEU	116	12.979	19.325	-9.129	1.00	17.60	ATOM	922	C	VAL	123	0.660	7.706	6.920	1.00	17.60
ATOM	838	CD2	LEU	116	11.228	21.010	-9.993	1.00	17.60	ATOM	923	O	VAL	123	1.090	7.095	7.154	1.00	17.60
ATOM	839	C	LEU	116	9.306	20.221	-6.014	1.00	17.60	ATOM	924	N	ALA	124	-0.195	7.000	7.953	1.00	17.60
ATOM	840	O	LEU	116	9.079	19.500	-5.132	1.00	17.60	ATOM	925	CA	ALA	124	0.253	0.111	9.316	1.00	17.60
ATOM	841	N	TYR	117	6.001	20.243	-6.005	1.00	17.60	ATOM	926	CB	ALA	124	-0.056	0.433	10.323	1.00	17.60
ATOM	842	CA	TYR	117	7.169	19.695	-5.041	1.00	17.60	ATOM	927	C	ALA	124	0.942	6.966	10.002	1.00	17.60



ATOM	908	O	ALA	124	1.619	7.100	11.015	1.00	17.60	16.509	-1.154	12.712	1.00	17.60
ATOM	909	K	GLY	125	0.003	5.703	9.411	1.00	17.60	16.411	-2.149	11.665	1.00	17.60
ATOM	910	CA	GLY	125	1.321	4.619	10.053	1.00	17.60	16.986	-1.999	10.469	1.00	17.60
ATOM	911	C	GLY	125	2.701	4.740	10.287	1.00	17.60	17.701	-0.934	10.429	1.00	17.60
ATOM	912	D	GLY	125	3.703	4.164	11.249	1.00	17.60	16.706	-2.931	9.564	1.00	17.60
ATOM	913	N	GLY	126	3.469	5.557	9.491	1.00	17.60	13.164	-1.092	15.641	1.00	17.60
ATOM	914	CA	GLY	126	4.895	5.672	9.620	1.00	17.60	13.719	-2.656	16.405	1.00	17.60
ATOM	915	C	GLY	126	5.471	4.501	0.071	1.00	17.60	12.160	-1.127	16.059	1.00	17.60
ATOM	916	O	GLY	126	6.193	3.589	0.397	1.00	17.60	11.617	-1.223	17.406	1.00	17.60
ATOM	917	N	GLU	127	6.778	4.543	0.708	1.00	17.50	10.571	-0.173	17.527	1.00	17.60
ATOM	918	CA	GLU	127	7.556	3.574	0.033	1.00	17.60	9.494	-0.106	10.601	1.00	17.60
ATOM	919	CB	GLU	127	9.012	4.010	0.130	1.00	17.60	0.306	0.224	17.697	1.00	17.60
ATOM	920	CG	GLU	127	9.290	5.212	7.223	1.00	17.60	7.109	0.047	10.299	1.00	17.60
ATOM	921	CD	GLU	127	10.662	5.063	7.388	1.00	17.60	5.033	0.517	17.943	1.00	17.60
ATOM	922	CE1	GLU	127	11.633	5.105	7.442	1.00	17.60	5.584	-0.425	16.990	1.00	17.60
ATOM	923	CE2	GLU	127	10.765	7.101	7.443	1.00	17.60	4.804	1.391	10.559	1.00	17.60
ATOM	924	C	GLU	127	7.371	2.126	0.480	1.00	17.60	11.043	-2.576	17.015	1.00	17.60
ATOM	925	O	GLU	127	6.912	1.040	9.590	1.00	17.60	11.221	-3.024	10.956	1.00	17.60
ATOM	926	N	HET	128	7.713	1.166	7.637	1.00	17.60	10.280	-3.230	16.935	1.00	17.60
ATOM	927	CA	HET	128	7.707	-0.227	0.017	1.00	17.60	9.737	-4.549	17.230	1.00	17.60
ATOM	928	CB	HET	128	7.739	-1.005	6.011	1.00	17.60	0.598	-0.700	16.165	1.00	17.60
ATOM	929	CG	HET	128	7.206	-2.477	6.900	1.00	17.60	0.175	-6.216	16.096	1.00	17.60
ATOM	930	SD	HET	128	0.115	-3.435	5.769	1.00	17.60	7.405	-3.902	16.497	1.00	17.60
ATOM	931	CE	HET	128	9.353	-3.652	6.997	1.00	17.60	6.259	-3.020	15.431	1.00	17.60
ATOM	932	C	HET	128	9.009	-0.304	0.750	1.00	17.60	10.079	-5.609	17.196	1.00	17.60
ATOM	933	O	HET	128	9.141	-1.290	0.560	1.00	17.60	10.020	-6.604	17.941	1.00	17.60
ATOM	934	N	PHE	129	10.012	0.450	0.478	1.00	17.60	11.928	-6.442	16.341	1.00	17.60
ATOM	935	CA	PHE	129	11.313	0.501	9.117	1.00	17.60	13.019	-7.406	14.993	1.00	17.60
ATOM	936	CB	PHE	129	12.147	1.571	0.430	1.00	17.60	11.094	-8.031	14.766	1.00	17.60
ATOM	937	CG	PHE	129	13.524	1.700	9.005	1.00	17.60	11.724	-9.123	13.039	1.00	17.60
ATOM	938	CD1	PHE	129	14.580	1.068	0.491	1.00	17.60	11.837	-10.485	14.474	1.00	17.60
ATOM	939	CD2	PHE	129	13.725	2.642	10.021	1.00	17.60	13.055	-11.340	14.677	1.00	17.60
ATOM	940	CE1	PHE	129	13.854	1.210	0.994	1.00	17.60	12.602	-12.629	15.406	1.00	17.60
ATOM	941	CE2	PHE	129	16.996	2.760	10.511	1.00	17.60	11.517	-13.314	14.691	1.00	17.60
ATOM	942	CE	PHE	129	16.067	2.067	10.010	1.00	17.60	11.090	-14.610	14.910	1.00	17.60
ATOM	943	C	PHE	129	11.246	0.708	10.592	1.00	17.60	11.635	-15.398	15.070	1.00	17.60
ATOM	944	O	PHE	129	11.741	-0.040	10.592	1.00	17.60	10.194	-15.262	14.101	1.00	17.60
ATOM	945	N	SER	130	10.709	1.916	11.339	1.00	17.60	10.254	-9.037	13.424	1.00	17.60
ATOM	946	CA	SER	130	10.641	2.290	12.412	1.00	17.60	9.444	-8.319	14.005	1.00	17.60
ATOM	947	CB	SER	130	9.702	3.527	12.527	1.00	17.60	9.033	-9.752	12.012	1.00	17.60
ATOM	948	CG	SER	130	9.929	4.402	11.497	1.00	17.60	0.445	-9.905	12.120	1.00	17.60
ATOM	949	C	SER	130	10.080	1.173	13.291	1.00	17.60	0.107	-9.239	10.771	1.00	17.60
ATOM	950	O	SER	130	10.646	0.049	14.325	1.00	17.60	7.903	-7.734	10.926	1.00	17.60
ATOM	951	N	HIS	131	9.014	0.494	12.917	1.00	17.60	0.339	-6.054	9.955	1.00	17.60
ATOM	952	CA	HIS	131	8.457	-0.405	13.671	1.00	17.60	7.325	-7.186	12.059	1.00	17.60
ATOM	953	CB	HIS	131	7.065	-0.060	13.271	1.00	17.60	0.204	-5.485	10.125	1.00	17.60
ATOM	954	CG	HIS	131	6.277	0.414	13.213	1.00	17.60	7.194	-5.016	12.225	1.00	17.60
ATOM	955	CD1	HIS	131	5.595	0.006	12.151	1.00	17.60	7.634	-4.960	11.250	1.00	17.60
ATOM	956	ND1	HIS	131	6.211	1.349	14.145	1.00	17.60	0.260	-11.492	12.120	1.00	17.60
ATOM	957	CE1	HIS	131	5.412	2.295	13.672	1.00	17.60	9.146	-12.246	11.034	1.00	17.60
ATOM	958	NE2	HIS	131	4.997	1.960	12.477	1.00	17.60	7.120	-11.054	12.617	1.00	17.60
ATOM	959	C	HIS	131	9.219	-1.094	13.447	1.00	17.60	6.779	-13.766	12.651	1.00	17.60
ATOM	960	O	HIS	131	9.201	-2.756	14.292	1.00	17.60	5.593	-13.527	13.505	1.00	17.60
ATOM	961	N	LEU	132	9.073	-2.149	12.335	1.00	17.60	4.707	-12.396	13.489	1.00	17.60
ATOM	962	CA	LEU	132	10.695	-3.319	12.198	1.00	17.60	3.114	-12.809	13.005	1.00	17.60
ATOM	963	CB	LEU	132	11.209	-3.405	10.776	1.00	17.60	2.286	-11.533	13.019	1.00	17.60
ATOM	964	CG	LEU	132	12.351	-4.312	10.401	1.00	17.60	2.744	-13.900	12.025	1.00	17.60
ATOM	965	CD1	LEU	132	11.060	-5.711	10.294	1.00	17.60	3.351	-13.492	15.324	1.00	17.60
ATOM	966	CD2	LEU	132	12.963	-3.026	9.110	1.00	17.60	6.433	-13.567	11.232	1.00	17.60
ATOM	967	C	LEU	132	11.014	-3.170	13.174	1.00	17.60	5.022	-12.756	10.537	1.00	17.60
ATOM	968	O	LEU	132	12.094	-4.018	13.923	1.00	17.60	6.713	-14.602	10.923	1.00	17.60
ATOM	969	N	ARG	133	12.543	-1.990	13.257	1.00	17.60	6.700	-15.280	9.565	1.00	17.60
ATOM	970	CA	ARG	133	13.645	-1.052	16.200	1.00	17.60	7.060	-16.779	9.650	1.00	17.60
ATOM	971	CB	ARG	133	14.381	-0.539	13.971	1.00	17.60					
ATOM	972	CG	ARG	133	15.244	-0.337	12.722	1.00	17.60					

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ATOM	1168	O	GLU	155	2.807	-6.420	-12.662	1.00	17.60	13.561	-1.899	-12.721	1.00	17.60
ATOM	1169	K	TYR	156	2.062	-5.494	-10.823	1.00	17.60	14.833	-2.255	-13.447	1.00	17.60
ATOM	1170	CA	TYR	156	1.463	-4.435	-11.570	1.00	17.60	11.328	-0.103	-11.702	1.00	17.60
ATOM	1171	CR	TYR	156	0.561	-3.767	-10.634	1.00	17.60	11.350	1.064	-12.040	1.00	17.60
ATOM	1172	CG	TYR	156	0.215	-2.367	-10.974	1.00	17.60	11.224	-0.445	-10.399	1.00	17.60
ATOM	1173	CD1	TYR	156	-0.719	-2.079	-11.965	1.00	17.60	11.163	0.473	-9.180	1.00	17.60
ATOM	1174	CE1	TYR	156	-1.057	-0.783	-12.210	1.00	17.60	9.987	-0.015	-8.232	1.00	17.60
ATOM	1175	CD2	TYR	156	0.828	-1.364	-10.228	1.00	17.60	9.937	0.522	-6.017	1.00	17.60
ATOM	1176	CE2	TYR	156	0.405	-0.062	-10.480	1.00	17.60	9.772	1.697	-6.534	1.00	17.60
ATOM	1177	CE	TYR	156	-0.450	0.201	-11.463	1.00	17.60	9.347	2.255	-5.269	1.00	17.60
ATOM	1178	OH	TYR	156	-0.811	1.513	-11.685	1.00	17.60	10.653	-0.091	-5.032	1.00	17.60
ATOM	1179	C	TYR	156	2.544	-3.525	-12.074	1.00	17.60	10.750	0.462	-4.501	1.00	17.60
ATOM	1180	O	TYR	156	2.595	-3.178	-13.236	1.00	17.60	10.105	1.631	-4.342	1.00	17.60
ATOM	1181	N	LEU	157	3.631	-3.330	-11.195	1.00	17.60	10.352	2.247	-3.156	1.00	17.60
ATOM	1182	CA	LEU	157	4.531	-2.289	-11.581	1.00	17.60	12.457	0.044	-0.557	1.00	17.60
ATOM	1183	CB	LEU	157	5.632	-2.099	-10.411	1.00	17.60	12.530	-1.313	-0.143	1.00	17.60
ATOM	1184	CG	LEU	157	5.032	-0.700	-10.023	1.00	17.60	13.483	0.835	-8.436	1.00	17.60
ATOM	1185	CD1	LEU	157	4.709	0.293	-10.069	1.00	17.60	14.671	0.185	-7.923	1.00	17.60
ATOM	1186	CD2	LEU	157	6.288	-0.791	-8.605	1.00	17.60	15.786	0.513	-0.065	1.00	17.60
ATOM	1187	C	LEU	157	5.349	-2.021	-12.736	1.00	17.60	15.477	-0.051	-10.220	1.00	17.60
ATOM	1188	O	LEU	157	5.091	-2.001	-12.340	1.00	17.60	16.388	0.546	-11.237	1.00	17.60
ATOM	1189	N	HIS	158	5.514	-4.109	-12.905	1.00	17.60	16.032	1.915	-11.467	1.00	17.60
ATOM	1190	CA	HIS	158	6.259	-4.639	-14.028	1.00	17.60	16.671	2.508	-12.376	1.00	17.60
ATOM	1191	CB	HIS	158	6.050	-5.970	-13.665	1.00	17.60	17.636	2.027	-13.074	1.00	17.60
ATOM	1192	CG	HIS	158	7.056	-5.734	-12.582	1.00	17.60	16.337	3.875	-12.593	1.00	17.60
ATOM	1193	CD1	HIS	158	8.360	-6.698	-11.767	1.00	17.60	15.056	0.509	-6.508	1.00	17.60
ATOM	1194	CD2	HIS	158	8.395	-4.570	-12.252	1.00	17.60	16.244	0.679	-6.261	1.00	17.60
ATOM	1195	CE1	HIS	158	9.209	-4.012	-11.260	1.00	17.60	14.375	0.593	-5.520	1.00	17.60
ATOM	1196	CE2	HIS	158	9.308	-6.086	-10.974	1.00	17.60	14.587	1.059	-6.206	1.00	17.60
ATOM	1197	C	HIS	158	5.452	-4.801	-15.296	1.00	17.60	14.533	2.584	-6.317	1.00	17.60
ATOM	1198	O	HIS	158	6.067	-4.713	-16.375	1.00	17.60	15.325	3.457	-3.337	1.00	17.60
ATOM	1199	N	SER	159	4.312	-5.008	-15.190	1.00	17.60	16.176	2.921	-2.596	1.00	17.60
ATOM	1200	CA	SER	159	3.258	-5.174	-16.373	1.00	17.60	15.007	4.601	-3.357	1.00	17.60
ATOM	1201	CB	SER	159	1.058	-5.491	-16.005	1.00	17.60	13.749	0.498	-3.051	1.00	17.60
ATOM	1202	CG	SER	159	1.435	-4.464	-15.164	1.00	17.60	13.250	1.172	-2.150	1.00	17.60
ATOM	1203	C	SER	159	3.216	-3.009	-17.170	1.00	17.60	13.514	-0.791	-3.054	1.00	17.60
ATOM	1204	O	SER	159	3.027	-3.912	-18.385	1.00	17.60	12.693	-1.403	-2.026	1.00	17.60
ATOM	1205	N	LEU	160	3.344	-2.776	-16.449	1.00	17.60	12.216	-2.786	-2.483	1.00	17.60
ATOM	1206	CA	LEU	160	3.573	-1.504	-17.076	1.00	17.60	11.150	-3.467	-1.691	1.00	17.60
ATOM	1207	CB	LEU	160	3.174	-0.523	16.107	1.00	17.60	9.846	-2.771	-1.918	1.00	17.60
ATOM	1208	CG	LEU	160	1.831	0.017	16.339	1.00	17.60	11.098	-6.926	-2.105	1.00	17.60
ATOM	1209	CD1	LEU	160	0.754	-0.946	16.568	1.00	17.60	11.629	-1.516	-0.037	1.00	17.60
ATOM	1210	CD2	LEU	160	1.744	0.594	-14.750	1.00	17.60	14.804	-1.887	-0.961	1.00	17.60
ATOM	1211	C	LEU	160	5.020	-1.241	-17.538	1.00	17.60	13.144	-1.028	0.283	1.00	17.60
ATOM	1212	O	LEU	160	5.369	-0.109	-17.069	1.00	17.60	13.020	-1.146	1.538	1.00	17.60
ATOM	1213	N	ASP	161	5.805	-2.264	-17.587	1.00	17.60	14.934	-0.130	1.663	1.00	17.60
ATOM	1214	CA	ASP	161	7.321	-2.104	-17.061	1.00	17.60	14.556	1.257	1.357	1.00	17.60
ATOM	1215	CB	ASP	161	7.514	-1.919	-19.329	1.00	17.60	15.812	2.011	1.457	1.00	17.60
ATOM	1216	CG	ASP	161	7.428	-3.242	-20.132	1.00	17.60	15.415	3.339	0.064	1.00	17.60
ATOM	1217	CD1	ASP	161	6.434	-3.353	-20.080	1.00	17.60	16.488	6.325	0.041	1.00	17.60
ATOM	1218	CD2	ASP	161	8.338	-8.134	-19.996	1.00	17.60	12.704	-0.036	2.487	1.00	17.60
ATOM	1219	C	ASP	161	8.223	-1.257	-17.020	1.00	17.60	11.789	-0.141	2.089	1.00	17.60
ATOM	1220	O	ASP	161	9.382	-0.957	-17.358	1.00	17.60	12.718	-1.316	3.724	1.00	17.60
ATOM	1221	N	LEU	162	7.677	-0.932	-15.837	1.00	17.60	13.423	-2.526	4.094	1.00	17.60
ATOM	1222	CA	LEU	162	8.346	-0.133	-14.865	1.00	17.60	11.930	-0.039	4.862	1.00	17.60
ATOM	1223	CB	LEU	162	7.376	0.501	-13.897	1.00	17.60	12.809	-1.287	5.970	1.00	17.60
ATOM	1224	CG	LEU	162	5.557	1.762	-14.141	1.00	17.60	13.033	-2.677	5.573	1.00	17.60
ATOM	1225	CD1	LEU	162	6.716	2.251	-15.513	1.00	17.60	11.503	0.606	4.989	1.00	17.60
ATOM	1226	CD2	LEU	162	5.100	1.486	-13.941	1.00	17.60	10.363	0.938	5.337	1.00	17.60
ATOM	1227	C	LEU	162	9.180	-1.161	-14.146	1.00	17.60	12.467	1.466	4.716	1.00	17.60
ATOM	1228	O	LEU	162	8.928	-2.378	-16.071	1.00	17.60	12.322	2.901	4.791	1.00	17.60
ATOM	1229	N	LEU	163	10.254	-0.594	-13.639	1.00	17.60	13.635	3.580	4.406	1.00	17.60
ATOM	1230	CA	LEU	163	11.202	-1.228	-12.758	1.00	17.60	14.871	2.236	5.295	1.00	17.60
ATOM	1231	CB	LEU	163	12.468	-1.694	-13.650	1.00	17.60	15.660	1.941	5.080	1.00	17.60
ATOM	1232	CG	LEU	163	12.878	-0.565	-16.669	1.00	17.60	15.103	0.075	4.938	1.00	17.60



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ATOM	1298	OE2	GIU	170	16.071	1.952	5.052	1.00	17.60	ATOM	1363	N	TIR	179	-1.598	-2.086	6.229	1.00	17.60
ATOM	1299	C	GIU	170	13.235	3.361	3.791	1.00	17.60	ATOM	1364	CA	TIR	179	-1.276	-2.498	6.866	1.00	17.60
ATOM	1300	O	GIU	170	10.130	3.518	6.234	1.00	17.60	ATOM	1365	CB	TIR	179	-2.423	-3.397	3.914	1.00	17.60
ATOM	1301	N	ASN	171	11.270	2.788	2.512	1.00	17.60	ATOM	1366	CC	TIR	179	-3.666	-3.507	3.962	1.00	17.60
ATOM	1302	CA	ASN	171	10.286	3.022	1.499	1.00	17.60	ATOM	1367	CD1	TIR	179	-3.534	-4.387	2.893	1.00	17.60
ATOM	1303	CB	ASN	171	10.843	2.985	0.192	1.00	17.60	ATOM	1368	CE1	TIR	179	-0.677	-5.397	2.843	1.00	17.60
ATOM	1304	CG	ASN	171	11.742	3.632	-0.370	1.00	17.60	ATOM	1369	CD2	TIR	179	-4.364	-3.648	3.007	1.00	17.60
ATOM	1305	OD1	ASN	171	12.265	4.468	0.357	1.00	17.60	ATOM	1370	CE2	TIR	179	-5.315	-4.656	4.966	1.00	17.60
ATOM	1306	ND2	ASN	171	12.026	3.594	-1.646	1.00	17.60	ATOM	1371	CH	TIR	179	-5.352	-5.510	3.884	1.00	17.60
ATOM	1307	C	ASN	171	0.079	2.436	1.628	1.00	17.60	ATOM	1372	OH	TIR	179	-6.287	-6.524	3.803	1.00	17.60
ATOM	1308	O	ASN	171	0.066	2.505	0.708	1.00	17.60	ATOM	1373	C	TIR	179	-0.259	-1.523	4.377	1.00	17.60
ATOM	1309	K	LEU	172	0.475	1.826	2.740	1.00	17.60	ATOM	1374	O	TIR	179	-0.275	-0.368	6.054	1.00	17.60
ATOM	1310	CA	LEU	172	7.169	1.223	2.798	1.00	17.60	ATOM	1375	N	ILE	180	0.615	-1.928	3.447	1.00	17.60
ATOM	1311	CR	LEU	172	7.342	-0.282	2.998	1.00	17.60	ATOM	1376	CA	ILE	180	1.719	-1.038	3.116	1.00	17.60
ATOM	1312	CG	LEU	172	0.137	-1.105	2.041	1.00	17.60	ATOM	1377	CB	ILE	180	3.079	-1.813	2.789	1.00	17.60
ATOM	1313	CD1	LEU	172	0.440	-2.407	2.555	1.00	17.60	ATOM	1378	CG2	ILE	180	3.542	-2.504	4.032	1.00	17.60
ATOM	1314	CD2	LEU	172	7.342	-1.141	0.851	1.00	17.60	ATOM	1379	CG3	ILE	180	2.964	-2.837	1.754	1.00	17.60
ATOM	1315	C	LEU	172	6.475	1.879	3.980	1.00	17.60	ATOM	1380	CD1	ILE	180	3.233	-2.787	0.337	1.00	17.60
ATOM	1316	O	LEU	172	7.055	1.795	5.034	1.00	17.60	ATOM	1381	C	ILE	180	1.320	-0.153	1.951	1.00	17.60
ATOM	1317	N	LEU	173	5.312	2.530	3.842	1.00	17.60	ATOM	1382	O	ILE	180	0.299	-0.366	1.310	1.00	17.60
ATOM	1318	CA	LEU	173	0.621	3.203	4.911	1.00	17.60	ATOM	1383	K	GLN	181	2.330	0.920	1.021	1.00	17.60
ATOM	1319	CB	LEU	173	4.125	4.557	4.496	1.00	17.60	ATOM	1384	CA	GLN	181	2.305	0.920	0.788	1.00	17.60
ATOM	1320	CG	LEU	173	5.064	5.707	4.199	1.00	17.60	ATOM	1385	CB	GLN	181	1.315	3.078	1.219	1.00	17.60
ATOM	1321	CD1	LEU	173	4.337	7.005	6.153	1.00	17.60	ATOM	1386	CC	GLN	181	-0.092	2.598	1.296	1.00	17.60
ATOM	1322	CD2	LEU	173	6.074	5.823	5.316	1.00	17.60	ATOM	1387	CD	GLN	181	-1.036	3.533	0.621	1.00	17.60
ATOM	1323	C	LEU	173	3.421	2.412	5.337	1.00	17.60	ATOM	1388	OE1	GLN	181	-0.071	6.749	0.672	1.00	17.60
ATOM	1324	O	LEU	173	2.822	1.806	4.443	1.00	17.60	ATOM	1389	NE2	GLN	181	-2.070	3.051	-0.039	1.00	17.60
ATOM	1325	H	ILE	174	3.010	2.393	6.825	1.00	17.60	ATOM	1390	C	GLN	181	3.514	2.414	0.471	1.00	17.60
ATOM	1326	CA	ILE	174	1.925	1.526	7.114	1.00	17.60	ATOM	1391	O	GLN	181	4.204	3.029	1.273	1.00	17.60
ATOM	1327	CB	ILE	174	2.240	1.013	8.504	1.00	17.60	ATOM	1392	H	VAL	182	3.925	1.970	-0.738	1.00	17.60
ATOM	1328	CD2	ILE	174	1.087	0.163	8.966	1.00	17.60	ATOM	1393	CA	VAL	182	5.164	2.312	-1.407	1.00	17.60
ATOM	1329	CG1	ILE	174	3.589	0.266	8.532	1.00	17.60	ATOM	1394	CB	VAL	182	5.381	1.435	-2.594	1.00	17.60
ATOM	1330	CD1	ILE	174	3.832	-0.952	7.620	1.00	17.60	ATOM	1395	CG1	VAL	182	6.841	1.481	-2.801	1.00	17.60
ATOM	1331	C	ILE	174	0.687	2.340	7.179	1.00	17.60	ATOM	1396	CG2	VAL	182	4.983	0.018	-2.415	1.00	17.60
ATOM	1332	O	ILE	174	0.802	3.453	7.668	1.00	17.60	ATOM	1397	C	VAL	182	5.111	1.768	-1.868	1.00	17.60
ATOM	1333	H	ASP	175	-0.466	1.893	6.714	1.00	17.60	ATOM	1398	O	VAL	182	4.377	4.292	-2.654	1.00	17.60
ATOM	1334	CA	ASP	175	-1.617	2.758	6.819	1.00	17.60	ATOM	1399	H	THR	183	5.978	4.464	-1.196	1.00	17.60
ATOM	1335	CB	ASP	175	-2.360	2.717	5.560	1.00	17.60	ATOM	1400	CA	THR	183	6.230	5.878	-1.358	1.00	17.60
ATOM	1336	CG	ASP	175	-2.020	1.380	5.195	1.00	17.60	ATOM	1401	CB	THR	183	6.387	6.401	0.101	1.00	17.60
ATOM	1337	OD1	ASP	175	-2.679	1.300	4.034	1.00	17.60	ATOM	1402	CG1	THR	183	6.318	7.834	0.076	1.00	17.60
ATOM	1338	OD2	ASP	175	-3.315	0.644	5.999	1.00	17.60	ATOM	1403	CG2	THR	183	7.663	5.870	0.743	1.00	17.60
ATOM	1339	C	ASP	175	-2.594	2.551	7.939	1.00	17.60	ATOM	1404	C	THR	183	7.499	5.919	-2.214	1.00	17.60
ATOM	1340	O	ASP	175	-2.246	1.740	8.772	1.00	17.60	ATOM	1405	O	THR	183	8.115	6.907	-2.484	1.00	17.60
ATOM	1341	H	GLN	176	-3.845	3.062	7.983	1.00	17.60	ATOM	1406	N	ASP	184	7.928	7.121	-2.695	1.00	17.60
ATOM	1342	CA	GLN	176	-4.774	2.924	9.098	1.00	17.60	ATOM	1407	CA	ASP	184	9.237	7.211	-3.312	1.00	17.60
ATOM	1343	CB	GLN	176	-5.698	4.137	9.197	1.00	17.60	ATOM	1408	CB	ASP	184	10.358	7.007	-2.297	1.00	17.60
ATOM	1344	CG	GLN	176	-6.594	4.105	10.456	1.00	17.60	ATOM	1409	CG	ASP	184	11.696	7.629	-2.733	1.00	17.60
ATOM	1345	CD	GLN	176	-7.023	5.030	10.567	1.00	17.60	ATOM	1410	OD1	ASP	184	12.108	8.669	-2.169	1.00	17.60
ATOM	1346	OE1	GLN	176	-7.785	5.989	11.347	1.00	17.60	ATOM	1411	OD2	ASP	184	12.327	7.064	-3.641	1.00	17.60
ATOM	1347	NE2	GLN	176	-8.960	6.788	9.885	1.00	17.60	ATOM	1412	C	ASP	184	9.512	6.249	-4.437	1.00	17.60
ATOM	1348	C	GLN	176	-5.589	1.690	8.896	1.00	17.60	ATOM	1413	O	ASP	184	9.890	5.099	-4.301	1.00	17.60
ATOM	1349	O	GLN	176	-6.818	1.669	8.869	1.00	17.60	ATOM	1414	N	PHE	185	9.406	6.906	-5.558	1.00	17.60
ATOM	1350	K	GLN	177	-4.846	0.626	8.708	1.00	17.60	ATOM	1415	CA	PHE	185	9.612	6.360	-6.849	1.00	17.60
ATOM	1351	CA	GLN	177	-5.374	-0.709	8.452	1.00	17.60	ATOM	1416	CB	PHE	185	8.399	6.721	-7.705	1.00	17.60
ATOM	1352	CB	GLN	177	-6.184	-0.823	7.082	1.00	17.60	ATOM	1417	CG	PHE	185	7.425	5.634	-7.618	1.00	17.60
ATOM	1353	CG	GLN	177	-7.706	-0.598	6.921	1.00	17.60	ATOM	1418	CD1	PHE	185	7.330	4.778	-8.693	1.00	17.60
ATOM	1354	CD	GLN	177	-8.531	-1.750	6.256	1.00	17.60	ATOM	1419	CD2	PHE	185	6.823	5.357	-6.419	1.00	17.60
ATOM	1355	OE1	GLN	177	-9.253	-1.506	5.275	1.00	17.60	ATOM	1420	CC1	PHE	185	6.631	3.635	-8.537	1.00	17.60
ATOM	1356	NE2	GLN	177	-8.566	-3.037	6.705	1.00	17.60	ATOM	1421	CC2	PHE	185	6.116	4.196	-6.264	1.00	17.60
ATOM	1357	C	GLN	177	-4.145	-1.651	8.183	1.00	17.60	ATOM	1422	C2	PHE	185	6.034	3.316	-7.319	1.00	17.60
ATOM	1358	O	GLN	177	-4.334	-2.809	8.001	1.00	17.60	ATOM	1423	C	PHE	185	10.288	6.918	-7.809	1.00	17.60
ATOM	1359	H	GLY	178	-2.891	-1.229	8.688	1.00	17.60	ATOM	1424	O	PHE	185	11.080	6.965	-8.622	1.00	17.60
ATOM	1360	CA	GLY	178	-1.720	-3.121	8.682	1.00	17.60	ATOM	1425	N	GLY	186	11.791	7.160	-5.533	1.00	17.60
ATOM	1361	C	GLY	178	-1.259	-2.752	7.366	1.00	17.60	ATOM	1426	CA	GLY	186	13.017	8.013	-6.900	1.00	17.60
ATOM	1362	O	GLY	178	-0.575	-2.799	7.418	1.00	17.60	ATOM	1427	C	GLY	186	13.804	7.255	-7.955	1.00	17.60

ATOM	1428	O	GLY	186	14.364	7.915	-8.007	3.00	17.60	19.008	-0.285	-23.016	1.00	17.60
ATOM	1429	N	PHE	187	13.897	5.919	-8.007	3.00	17.60	19.297	-2.153	-19.039	1.00	17.60
ATOM	1430	CA	PHE	187	14.601	5.365	-9.322	3.00	17.60	19.010	-1.255	-20.639	1.00	17.60
ATOM	1431	CB	PHE	187	15.637	6.456	-8.587	3.00	17.60	18.078	-1.051	-18.683	1.00	17.60
ATOM	1432	CC	PHE	187	16.700	5.284	-7.954	3.00	17.60	19.282	-0.491	-18.361	1.00	17.60
ATOM	1433	CD	PHE	187	17.129	6.419	-8.520	3.00	17.60	18.109	0.233	-17.582	1.00	17.60
ATOM	1434	CE	PHE	187	17.191	4.966	-6.761	3.00	17.60	18.490	1.597	-17.454	1.00	17.60
ATOM	1435	CE1	PHE	187	18.042	7.225	-7.889	3.00	17.60	17.799	-0.356	-16.218	1.00	17.60
ATOM	1436	CE2	PHE	187	18.103	5.731	-6.110	3.00	17.60	20.561	-0.687	-17.539	1.00	17.60
ATOM	1437	CE	PHE	187	18.537	6.089	-6.670	3.00	17.60	20.950	-1.023	-17.194	1.00	17.60
ATOM	1438	C	PHE	187	13.699	4.673	-10.094	1.00	17.60	21.207	0.447	-17.274	1.00	17.60
ATOM	1439	O	PHE	187	14.208	3.926	-10.910	1.00	17.60	22.534	0.428	-16.720	1.00	17.60
ATOM	1440	N	ALA	188	12.385	6.917	-10.091	1.00	17.60	23.541	0.692	-17.076	1.00	17.60
ATOM	1441	CA	ALA	188	11.455	4.171	-10.917	1.00	17.60	23.765	-0.441	-18.063	1.00	17.60
ATOM	1442	CB	ALA	188	10.072	4.600	-10.621	1.00	17.60	23.156	-0.589	-20.050	1.00	17.60
ATOM	1443	C	ALA	188	11.737	4.425	-12.371	1.00	17.60	23.633	-1.018	-20.452	1.00	17.60
ATOM	1444	O	ALA	188	12.142	5.570	-12.669	1.00	17.60	22.265	0.119	-20.841	1.00	17.60
ATOM	1445	N	LYS	189	11.611	3.537	-13.330	1.00	17.60	24.571	-1.492	-18.571	1.00	17.60
ATOM	1446	CA	LYS	189	11.986	3.031	-14.684	1.00	17.60	24.459	-2.321	-19.557	1.00	17.60
ATOM	1447	CB	LYS	189	13.532	3.536	-14.873	1.00	17.60	23.249	-2.394	-21.635	1.00	17.60
ATOM	1448	CG	LYS	189	14.124	3.032	-16.269	1.00	17.60	21.067	-0.465	-22.047	1.00	17.60
ATOM	1449	CD	LYS	189	15.612	3.934	-16.303	1.00	17.60	22.355	-1.708	-22.431	1.00	17.60
ATOM	1450	CE	LYS	189	16.120	4.237	-17.690	1.00	17.60	22.023	1.384	-25.567	1.00	17.60
ATOM	1451	CE1	LYS	189	15.663	5.500	-18.226	1.00	17.60	21.837	3.911	-33.599	1.00	17.60
ATOM	1452	C	LYS	189	11.124	2.966	-15.569	1.00	17.60	20.785	6.518	-34.800	1.00	17.60
ATOM	1453	O	LYS	189	10.911	1.801	-15.243	1.00	17.60	19.404	4.308	-35.392	1.00	17.60
ATOM	1454	N	ARG	190	10.559	3.539	-16.639	1.00	17.60	18.303	6.976	-36.676	1.00	17.60
ATOM	1455	CA	ARG	190	9.803	2.726	-17.556	1.00	17.60	19.173	2.075	-35.341	1.00	17.60
ATOM	1456	CB	ARG	190	8.757	3.613	-18.208	1.00	17.60	18.398	5.000	-34.424	1.00	17.60
ATOM	1457	CD	ARG	190	7.847	2.691	-19.029	1.00	17.60	21.529	0.965	-32.542	1.00	17.60
ATOM	1458	CE	ARG	190	6.387	3.051	-19.316	1.00	17.60	22.722	2.265	-32.616	1.00	17.60
ATOM	1459	CE1	ARG	190	6.243	2.826	-20.731	1.00	17.60	22.056	1.332	-32.218	1.00	17.60
ATOM	1460	CE2	ARG	190	5.277	2.164	-21.314	1.00	17.60	23.020	2.581	-31.037	1.00	17.60
ATOM	1461	CE3	ARG	190	4.285	1.604	-20.639	1.00	17.60	24.011	1.956	-30.630	1.00	17.60
ATOM	1462	CE4	ARG	190	5.353	2.110	-22.627	1.00	17.60	25.457	1.970	-30.093	1.00	17.60
ATOM	1463	O	ARG	190	10.819	2.101	-18.542	1.00	17.60	25.790	1.029	-8.044	1.00	17.60
ATOM	1464	C	ARG	190	11.256	2.944	-19.388	1.00	17.60	26.706	-0.165	-9.175	1.00	17.60
ATOM	1465	N	VAL	191	11.324	0.968	-18.484	1.00	17.60	26.508	1.905	-7.027	1.00	17.60
ATOM	1466	CA	VAL	191	12.278	0.554	-19.480	1.00	17.60	23.235	2.064	-9.714	1.00	17.60
ATOM	1467	CB	VAL	191	13.690	0.066	-19.118	1.00	17.60	23.519	4.056	-9.639	1.00	17.60
ATOM	1468	CG	VAL	191	14.404	1.268	-18.794	1.00	17.60	22.164	2.315	-9.157	1.00	17.60
ATOM	1469	CD	VAL	191	13.405	-0.841	-17.946	1.00	17.60	21.362	3.034	-8.179	1.00	17.60
ATOM	1470	C	VAL	191	11.722	-0.691	-20.031	1.00	17.60	20.496	6.099	-8.072	1.00	17.60
ATOM	1471	O	VAL	191	11.328	-1.638	-19.334	1.00	17.60	19.489	3.416	-10.182	1.00	17.60
ATOM	1472	N	LYE	192	11.757	-0.678	-21.355	1.00	17.60	20.517	1.939	-7.527	1.00	17.60
ATOM	1473	CA	LYS	192	11.205	-1.063	-22.010	1.00	17.60	20.264	0.067	-8.150	1.00	17.60
ATOM	1474	CB	LYS	192	10.357	-1.484	-23.144	1.00	17.60	20.212	2.218	-6.235	1.00	17.60
ATOM	1475	CG	LYS	192	9.499	-2.664	-23.563	1.00	17.60	19.421	1.400	-5.333	1.00	17.60
ATOM	1476	CD	LYS	192	8.442	-2.034	-24.415	1.00	17.60	19.950	1.655	-3.920	1.00	17.60
ATOM	1477	CE	LYS	192	7.131	-1.894	-23.730	1.00	17.60	20.649	2.665	-3.762	1.00	17.60
ATOM	1478	CE1	LYS	192	7.259	-1.140	-22.516	1.00	17.60	19.715	0.371	-2.071	1.00	17.60
ATOM	1479	C	LYS	192	12.492	-2.606	-22.499	1.00	17.60	20.327	1.276	-1.501	1.00	17.60
ATOM	1480	O	LYS	192	12.085	-3.040	-23.629	1.00	17.60	19.230	1.276	-0.400	1.00	17.60
ATOM	1481	N	GLY	193	13.523	-2.824	-21.676	1.00	17.60	18.496	2.469	-0.759	1.00	17.60
ATOM	1482	CA	GLY	193	14.720	-3.524	-22.136	1.00	17.60	19.781	1.211	0.922	1.00	17.60
ATOM	1483	C	GLY	193	15.583	-3.781	-20.927	1.00	17.60	21.298	0.015	-1.279	1.00	17.60
ATOM	1484	O	GLY	193	15.118	-4.209	-19.852	1.00	17.60	20.080	-1.094	-1.352	1.00	17.60
ATOM	1485	N	ARG	194	16.823	-3.393	-21.137	1.00	17.60	22.516	0.199	-0.914	1.00	17.60
ATOM	1486	CA	ARG	194	17.078	-3.572	-20.168	1.00	17.60	23.092	1.469	-0.483	1.00	17.60
ATOM	1487	CB	ARG	194	18.034	-4.371	-20.795	1.00	17.60	23.543	-0.066	-0.070	1.00	17.60
ATOM	1488	CG	ARG	194	18.034	-4.889	-22.302	1.00	17.60	24.616	-0.340	0.037	1.00	17.60
ATOM	1489	CD	ARG	194	19.128	-3.977	-23.579	1.00	17.60	24.570	1.114	-0.345	1.00	17.60
ATOM	1490	CE	ARG	194	18.904	-2.529	-23.379	1.00	17.60					
ATOM	1491	CE1	ARG	194	19.206	-1.549	-24.256	1.00	17.60					
ATOM	1492	NH1	ARG	194	19.757	-1.773	-25.484	1.00	17.60					



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ATOM	1550	C	PRO	202	23.157	-2.760	-0.400	1.00	17.60	1673	CD1	ILE	210	29.662	-5.033	-6.015	1.00	17.60
ATOM	1559	O	PRO	202	23.356	-3.157	-1.270	1.00	17.60	1626	C	ILE	210	20.381	-4.708	-9.764	1.00	17.60
ATOM	1560	N	GIU	203	22.525	-2.581	0.646	1.00	17.60	1625	O	ILE	210	29.454	-4.186	-10.090	1.00	17.60
ATOM	1561	CA	GIU	203	22.258	-3.989	0.997	1.00	17.60	1626	N	ILE	211	28.106	-5.964	-10.156	1.00	17.60
ATOM	1562	CB	GIU	203	21.902	-4.183	2.507	1.00	17.60	1627	CA	ILE	211	29.045	-6.491	-11.203	1.00	17.60
ATOM	1563	CG	GIU	203	21.311	-3.024	3.263	1.00	17.60	1628	CB	ILE	211	28.979	-7.970	-11.168	1.00	17.60
ATOM	1564	CD	GIU	203	22.311	-1.990	3.776	1.00	17.60	1629	CG	ILE	211	30.016	-8.790	-10.509	1.00	17.60
ATOM	1565	OE1	GIU	203	22.769	-2.189	4.899	1.00	17.60	1630	CD1	ILE	211	31.005	-7.998	-9.705	1.00	17.60
ATOM	1566	OE2	GIU	203	22.597	-1.002	3.099	1.00	17.60	1631	CD2	ILE	211	29.239	-9.772	-9.709	1.00	17.60
ATOM	1567	C	GIU	203	21.155	-4.641	0.191	1.00	17.60	1632	C	ILE	211	28.310	-5.930	-12.426	1.00	17.60
ATOM	1568	O	GLU	203	20.910	-3.951	0.231	1.00	17.60	1633	O	ILE	211	27.566	-6.706	-13.033	1.00	17.60
ATOM	1569	N	TIR	204	20.404	-3.743	-0.506	1.00	17.60	1634	N	SER	212	26.460	-4.643	-12.792	1.00	17.60
ATOM	1570	CA	TIR	204	19.303	-6.131	-1.320	1.00	17.60	1635	CA	SER	212	27.570	-3.987	-13.749	1.00	17.60
ATOM	1571	CB	TIR	204	18.334	-2.999	-1.302	1.00	17.60	1636	CB	SER	212	27.958	-2.495	-13.812	1.00	17.60
ATOM	1572	CG	TIR	204	17.497	-3.272	-0.063	1.00	17.60	1637	CG	SER	212	29.350	-2.146	-13.783	1.00	17.60
ATOM	1573	CD1	TIR	204	16.576	-4.312	-0.091	1.00	17.60	1638	C	SER	212	27.352	-4.908	-15.174	1.00	17.60
ATOM	1574	CE1	TIR	204	15.933	-6.696	1.078	1.00	17.60	1639	O	SER	212	28.027	-4.155	-16.132	1.00	17.60
ATOM	1575	CD2	TIR	204	17.766	-2.601	1.142	1.00	17.60	1640	N	LYS	213	26.355	-5.367	-15.333	1.00	17.60
ATOM	1576	CE2	TIR	204	17.096	-2.995	2.309	1.00	17.60	1641	CA	LYS	213	26.003	-6.307	-16.542	1.00	17.60
ATOM	1577	CG	TIR	204	16.201	-4.013	2.265	1.00	17.60	1642	CB	LYS	213	26.000	-7.577	-16.147	1.00	17.60
ATOM	1578	OH	TIR	204	15.501	-4.657	3.408	1.00	17.60	1643	CG	LYS	213	27.382	-0.055	-15.687	1.00	17.60
ATOM	1579	C	TIR	204	19.077	-4.427	-2.708	1.00	17.60	1644	CD	LYS	213	27.370	-9.314	-14.813	1.00	17.60
ATOM	1580	O	TIR	204	19.171	-5.107	-3.439	1.00	17.60	1645	CE	LYS	213	26.164	-10.376	-15.409	1.00	17.60
ATOM	1581	N	ILE	205	21.077	-3.985	-3.124	1.00	17.60	1646	NE	LYS	213	26.596	-11.666	-16.795	1.00	17.60
ATOM	1582	CA	ILE	205	21.511	-4.134	-4.497	1.00	17.60	1647	C	LYS	213	24.655	-5.740	-17.235	1.00	17.60
ATOM	1583	CB	ILE	205	22.860	-3.478	-6.604	1.00	17.60	1648	O	LYS	213	24.246	-6.439	-18.386	1.00	17.60
ATOM	1584	CG	ILE	205	23.128	-2.133	-5.266	1.00	17.60	1649	N	GLY	214	23.926	-4.657	-16.893	1.00	17.60
ATOM	1585	CD1	ILE	205	21.059	-1.372	-5.282	1.00	17.60	1650	CA	GLY	214	22.655	-4.464	-17.551	1.00	17.60
ATOM	1586	CD2	ILE	205	24.309	-1.460	-4.622	1.00	17.60	1651	C	GLY	214	21.666	-5.376	-16.859	1.00	17.60
ATOM	1587	C	ILE	205	21.559	-5.594	-4.916	1.00	17.60	1652	O	GLY	214	21.833	-6.385	-16.603	1.00	17.60
ATOM	1588	O	ILE	205	21.056	-6.489	-4.127	1.00	17.60	1653	N	TIR	215	20.614	-6.688	-16.458	1.00	17.60
ATOM	1589	N	ALA	206	21.087	-5.838	-6.143	1.00	17.60	1654	CA	TIR	215	19.646	-5.310	-15.619	1.00	17.60
ATOM	1590	CA	ALA	206	21.160	-7.153	-6.746	1.00	17.60	1655	CB	TIR	215	19.937	-4.083	-14.156	1.00	17.60
ATOM	1591	CB	ALA	206	20.100	-7.216	-7.850	1.00	17.60	1656	CG	TIR	215	20.034	-3.384	-13.771	1.00	17.60
ATOM	1592	C	ALA	206	22.556	-7.266	-7.296	1.00	17.60	1657	CD1	TIR	215	18.955	-2.853	-13.164	1.00	17.60
ATOM	1593	O	ALA	206	23.013	-6.155	-7.615	1.00	17.60	1658	CB1	TIR	215	18.911	-1.569	-12.743	1.00	17.60
ATOM	1594	N	PRO	207	23.262	-8.404	-7.472	1.00	17.60	1659	CD2	TIR	215	21.120	-2.563	-13.960	1.00	17.60
ATOM	1595	CD	PRO	207	22.622	-9.695	-7.672	1.00	17.60	1660	CE2	TIR	215	21.081	-1.228	-13.542	1.00	17.60
ATOM	1596	CA	PRO	207	24.675	-8.524	-7.827	1.00	17.60	1661	CG	TIR	215	19.949	-0.758	-12.930	1.00	17.60
ATOM	1597	CB	PRO	207	25.063	-9.914	-7.566	1.00	17.60	1662	OH	TIR	215	19.756	0.537	-12.105	1.00	17.60
ATOM	1598	CG	PRO	207	23.756	-10.662	-7.352	1.00	17.60	1663	C	TIR	215	18.269	-4.930	-16.107	1.00	17.60
ATOM	1599	O	PRO	207	24.999	-8.193	-9.289	1.00	17.60	1664	O	TIR	215	18.007	-4.081	-16.966	1.00	17.60
ATOM	1600	O	PRO	207	26.123	-7.789	-9.592	1.00	17.60	1665	N	ASH	216	17.345	-5.574	-15.675	1.00	17.60
ATOM	1601	N	GLU	208	24.034	-8.322	-10.214	1.00	17.60	1666	CA	ASH	216	15.985	-5.509	-15.915	1.00	17.60
ATOM	1602	CA	GLU	208	24.253	-7.872	-11.546	1.00	17.60	1667	CB	ASH	216	15.806	-6.618	-16.901	1.00	17.60
ATOM	1603	CB	GLU	208	23.118	-8.277	-12.480	1.00	17.60	1668	CG	ASH	216	16.398	-7.924	-16.334	1.00	17.60
ATOM	1604	CG	GLU	208	21.773	-7.703	-12.166	1.00	17.60	1669	OD1	ASH	216	16.693	-8.078	-15.137	1.00	17.60
ATOM	1605	CD	GLU	208	20.791	-8.657	-11.532	1.00	17.60	1670	ND2	ASH	216	16.658	-8.086	-17.198	1.00	17.60
ATOM	1606	OE1	GLU	208	19.582	-8.489	-11.672	1.00	17.60	1671	C	ASH	216	15.153	-5.733	-14.669	1.00	17.60
ATOM	1607	OE2	GLU	208	21.237	-9.593	-10.890	1.00	17.60	1672	O	ASH	216	15.663	-5.836	-13.510	1.00	17.60
ATOM	1608	C	GLU	208	24.369	-6.368	-11.527	1.00	17.60	1673	N	LYS	217	13.889	-6.836	-14.914	1.00	17.60
ATOM	1609	O	GLU	208	24.954	-5.809	-12.441	1.00	17.60	1674	CA	LYS	217	12.857	-6.326	-13.994	1.00	17.60
ATOM	1610	N	ILE	209	23.803	-5.605	-10.563	1.00	17.60	1675	CB	LYS	217	11.612	-7.037	-14.631	1.00	17.60
ATOM	1611	CA	ILE	209	24.037	-6.178	-10.681	1.00	17.60	1676	CG	LYS	217	11.066	-6.652	-16.021	1.00	17.60
ATOM	1612	CB	ILE	209	23.019	-3.466	-9.026	1.00	17.60	1677	CD	LYS	217	10.678	-5.164	-16.061	1.00	17.60
ATOM	1613	CG1	ILE	209	23.132	-1.955	-9.969	1.00	17.60	1678	CE	LYS	217	11.315	-4.316	-17.221	1.00	17.60
ATOM	1614	CG1	ILE	209	21.656	-3.963	-10.252	1.00	17.60	1679	N2	LYS	217	12.779	-4.482	-17.387	1.00	17.60
ATOM	1615	CD1	ILE	209	20.589	-3.274	-9.398	1.00	17.60	1680	C	LYS	217	13.337	-7.246	-12.914	1.00	17.60
ATOM	1616	C	ILE	209	25.419	-3.790	-10.264	1.00	17.60	1681	O	LYS	217	12.702	-7.150	-13.869	1.00	17.60
ATOM	1617	O	ILE	209	25.930	-2.849	-10.853	1.00	17.60	1682	N	ALA	218	14.381	-8.079	-13.100	1.00	17.60
ATOM	1618	N	ILE	210	26.065	-6.445	-9.290	1.00	17.60	1683	CA	ALA	218	14.771	-9.089	-12.135	1.00	17.60
ATOM	1619	CA	ILE	210	27.371	-3.929	-8.925	1.00	17.60	1684	CB	ALA	218	15.675	-10.083	-12.804	1.00	17.60
ATOM	1620	CB	ILE	210	27.675	-4.023	-7.360	1.00	17.60	1685	C	ALA	218	15.462	-8.567	-10.886	1.00	17.60
ATOM	1621	CG1	ILE	210	26.613	-8.151	-6.511	1.00	17.60	1686	O	ALA	218	15.548	-9.254	-9.850	1.00	17.60
ATOM	1622	CG1	ILE	210	28.514	-5.238	-7.862	1.00	17.60	1687	N	VAL	219	15.981	-7.300	-10.952	1.00	17.60

ATOM	1688	CA	VAL	219	16.693	-6.609	-9.787	1.00	17.60	15.127	-0.756	2.915	1.00	17.60
ATOM	1689	CB	VAL	219	17.088	-5.299	-9.997	1.00	17.60	13.935	-7.855	1.335	1.00	17.60
ATOM	1690	CG1	VAL	219	18.182	-5.527	-10.951	1.00	17.60	12.917	-7.604	2.235	1.00	17.60
ATOM	1691	CG2	VAL	219	16.118	-6.231	-10.475	1.00	17.60	11.758	-6.862	3.546	1.00	17.60
ATOM	1692	C	VAL	219	15.420	-6.511	-8.736	1.00	17.60	10.845	-6.168	2.472	1.00	17.60
ATOM	1693	O	VAL	219	15.682	-6.634	-7.532	1.00	17.60	11.431	-4.853	2.831	1.00	17.60
ATOM	1694	N	ASP	220	16.182	-6.314	-9.165	1.00	17.60	9.557	-5.881	1.814	1.00	17.60
ATOM	1695	CA	ASP	220	13.121	-6.116	-8.224	1.00	17.60	12.429	-8.573	3.039	1.00	17.60
ATOM	1696	CB	ASP	220	11.862	-5.622	-8.950	1.00	17.60	12.454	-8.492	4.255	1.00	17.60
ATOM	1697	CG	ASP	220	11.891	-4.095	-9.382	1.00	17.60	12.066	-9.708	2.469	1.00	17.60
ATOM	1698	CG1	ASP	220	12.629	-3.655	-10.036	1.00	17.60	11.512	-10.836	3.225	1.00	17.60
ATOM	1699	CG2	ASP	220	11.183	-3.318	-8.536	1.00	17.60	11.123	-12.015	2.287	1.00	17.60
ATOM	1700	C	ASP	220	12.855	-7.400	-7.693	1.00	17.60	10.621	-11.152	3.135	1.00	17.60
ATOM	1701	O	ASP	220	12.293	-7.339	-6.404	1.00	17.60	9.973	-11.655	1.961	1.00	17.60
ATOM	1702	N	TRP	221	13.215	-8.568	-7.964	1.00	17.60	9.616	-12.704	0.299	1.00	17.60
ATOM	1703	CA	TRP	221	12.892	-9.736	-7.235	1.00	17.60	12.505	-11.325	6.256	1.00	17.60
ATOM	1704	CB	TRP	221	12.618	-10.867	-8.137	1.00	17.60	12.083	-11.642	5.341	1.00	17.60
ATOM	1705	CG	TRP	221	13.309	-10.554	-8.782	1.00	17.60	13.797	-11.388	6.025	1.00	17.60
ATOM	1706	CG1	TRP	221	10.063	-10.346	-8.240	1.00	17.60	14.755	-11.843	4.987	1.00	17.60
ATOM	1707	CG2	TRP	221	9.339	-10.089	-9.383	1.00	17.60	16.053	-12.035	6.312	1.00	17.60
ATOM	1708	CE1	TRP	221	9.313	-10.317	-7.052	1.00	17.60	17.190	-12.623	5.093	1.00	17.60
ATOM	1709	CE2	TRP	221	11.349	-10.436	-10.306	1.00	17.60	17.769	-12.048	6.189	1.00	17.60
ATOM	1710	CE3	TRP	221	10.126	-10.135	-10.432	1.00	17.60	18.079	-12.635	6.743	1.00	17.60
ATOM	1711	CE4	TRP	221	7.994	-9.810	-9.433	1.00	17.60	17.708	-13.784	4.578	1.00	17.60
ATOM	1712	CE5	TRP	221	8.005	-10.037	-7.070	1.00	17.60	18.803	-14.386	5.125	1.00	17.60
ATOM	1713	CE6	TRP	221	7.312	-9.786	-8.241	1.00	17.60	19.388	-13.793	6.194	1.00	17.60
ATOM	1714	C	TRP	221	13.947	-10.105	-6.287	1.00	17.60	20.573	-14.356	6.616	1.00	17.60
ATOM	1715	O	TRP	221	13.571	-10.661	-5.248	1.00	17.60	14.091	-10.782	6.086	1.00	17.60
ATOM	1716	N	TRP	222	15.207	-9.748	-6.595	1.00	17.60	14.986	-11.307	7.228	1.00	17.60
ATOM	1717	CA	TRP	222	16.292	-9.946	-5.638	1.00	17.60	15.215	-8.531	5.976	1.00	17.60
ATOM	1718	CB	TRP	222	17.664	-9.488	-6.138	1.00	17.60	15.285	-7.201	5.856	1.00	17.60
ATOM	1719	CG	TRP	222	18.822	-9.618	-5.173	1.00	17.60	15.172	-5.709	6.007	1.00	17.60
ATOM	1720	CG1	TRP	222	19.762	-10.596	-5.142	1.00	17.60	16.309	-4.864	6.559	1.00	17.60
ATOM	1721	CG2	TRP	222	20.682	-10.127	-4.192	1.00	17.60	17.092	-4.267	5.813	1.00	17.60
ATOM	1722	CE1	TRP	222	20.034	-11.777	-5.757	1.00	17.60	16.353	-4.754	7.773	1.00	17.60
ATOM	1723	CE2	TRP	222	19.125	-8.637	-4.272	1.00	17.60	14.158	-8.448	7.669	1.00	17.60
ATOM	1724	CE3	TRP	222	20.219	-8.957	-3.691	1.00	17.60	14.163	-8.531	8.865	1.00	17.60
ATOM	1725	CE4	TRP	222	21.779	-10.825	-3.855	1.00	17.60	12.210	-8.506	7.203	1.00	17.60
ATOM	1726	CE5	TRP	222	21.165	-12.481	-5.423	1.00	17.60	11.754	-8.524	8.073	1.00	17.60
ATOM	1727	CE6	TRP	222	22.012	-12.018	-4.482	1.00	17.60	10.508	-8.583	7.237	1.00	17.60
ATOM	1728	C	TRP	222	15.917	-9.088	-6.419	1.00	17.60	10.214	-7.355	6.413	1.00	17.60
ATOM	1729	O	TRP	222	15.795	-9.674	-3.342	1.00	17.60	8.603	-7.416	5.592	1.00	17.60
ATOM	1730	N	ALA	223	15.760	-7.761	-6.538	1.00	17.60	9.024	-8.484	4.278	1.00	17.60
ATOM	1731	CA	ALA	223	15.375	-6.950	-3.399	1.00	17.60	11.783	-9.700	9.029	1.00	17.60
ATOM	1732	CB	ALA	223	15.127	-5.547	-3.843	1.00	17.60	11.784	-9.434	10.207	1.00	17.60
ATOM	1733	C	ALA	223	14.115	-7.495	-2.705	1.00	17.60	11.849	-10.972	8.621	1.00	17.60
ATOM	1734	O	ALA	223	14.101	-7.476	-1.482	1.00	17.60	11.867	-12.131	9.508	1.00	17.60
ATOM	1735	N	LEU	224	13.069	-8.096	-3.274	1.00	17.60	11.626	-13.128	8.744	1.00	17.60
ATOM	1736	CA	LEU	224	11.974	-8.685	-2.486	1.00	17.60	13.133	-12.352	10.303	1.00	17.60
ATOM	1737	CB	LEU	224	10.937	-9.485	-3.241	1.00	17.60	13.076	-12.872	11.426	1.00	17.60
ATOM	1738	CG	LEU	224	9.485	-9.501	-2.844	1.00	17.60	14.306	-12.048	9.752	1.00	17.60
ATOM	1739	CG1	LEU	224	8.965	-10.836	-3.302	1.00	17.60	15.523	-12.212	10.519	1.00	17.60
ATOM	1740	CG2	LEU	224	9.261	-9.281	-1.373	1.00	17.60	16.732	-12.390	9.667	1.00	17.60
ATOM	1741	C	LEU	224	12.550	-9.740	-1.578	1.00	17.60	15.874	-13.065	12.426	1.00	17.60
ATOM	1742	O	LEU	224	12.169	-9.823	-0.424	1.00	17.60	16.606	-13.314	12.371	1.00	17.60
ATOM	1743	N	GLY	225	13.676	-10.529	-2.085	1.00	17.60	15.125	-9.830	11.189	1.00	17.60
ATOM	1744	CA	GLY	225	14.103	-11.582	-1.294	1.00	17.60	15.777	-8.652	12.007	1.00	17.60
ATOM	1745	C	GLY	225	14.813	-10.920	-0.130	1.00	17.60	16.903	-7.776	11.438	1.00	17.60
ATOM	1746	O	GLY	225	14.956	-11.510	0.918	1.00	17.60	17.185	-6.645	11.064	1.00	17.60
ATOM	1747	N	VAL	226	15.224	-9.667	-0.270	1.00	17.60	17.514	-8.336	10.415	1.00	17.60
ATOM	1748	CA	VAL	226	15.967	-9.059	0.807	1.00	17.60	18.657	-7.705	9.737	1.00	17.60
ATOM	1749	CB	VAL	226	16.941	-8.010	0.214	1.00	17.60	19.921	-7.936	10.566	1.00	17.60
ATOM	1750	CG1	VAL	226	17.879	-7.675	1.347	1.00	17.60	20.359	-9.387	10.834	1.00	17.60
ATOM	1751	CG2	VAL	226	17.862	-8.608	-0.901	1.00	17.60	19.731	-9.817	12.063	1.00	17.60
ATOM	1752	C	VAL	226	14.987	-8.492	1.772	1.00	17.60					

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ATOM	1818	CEL TYR	235	19.064	-11.132	32.322	1.00	17.60	ATOM	1883	N	PRO	263	29.077	0.216	2.559	1.00	17.60
ATOM	1819	CD2 TYR	235	20.710	-10.222	9.000	1.00	17.60	ATOM	1884	CD	PRO	263	29.093	1.599	2.184	1.00	17.60
ATOM	1820	CE2 TYR	235	20.826	-11.549	10.153	1.00	17.60	ATOM	1885	CA	PRO	263	29.018	-0.521	1.600	1.00	17.60
ATOM	1821	CE TYR	235	20.378	-11.957	11.393	1.00	17.60	ATOM	1886	CB	PRO	263	28.497	0.532	0.678	1.00	17.60
ATOM	1822	ON TYR	235	20.512	-13.250	11.795	1.00	17.60	ATOM	1887	CG	PRO	243	28.534	1.775	1.493	1.00	17.60
ATOM	1823	C TYR	235	16.009	-8.172	8.273	1.00	17.60	ATOM	1888	C	PRO	243	29.910	-1.511	0.869	1.00	17.60
ATOM	1824	O TYR	235	18.316	-9.177	7.041	1.00	17.60	ATOM	1889	O	PRO	243	29.514	-2.678	0.777	1.00	17.60
ATOM	1825	N PRO	236	19.715	-7.471	7.462	1.00	17.60	ATOM	1890	N	ILE	244	31.105	-1.388	0.416	1.00	17.60
ATOM	1826	CD PRO	236	20.383	-6.191	7.706	1.00	17.60	ATOM	1891	CA	ILE	244	32.047	-2.051	-0.289	1.00	17.60
ATOM	1827	CA PRO	236	19.963	-7.777	6.097	1.00	17.60	ATOM	1892	CB	ILE	244	33.420	-1.276	-0.286	1.00	17.60
ATOM	1828	CB PRO	236	20.165	-6.562	5.648	1.00	17.60	ATOM	1893	CG2	ILE	244	34.314	-1.396	0.946	1.00	17.60
ATOM	1829	CG PRO	236	20.354	-5.032	6.426	1.00	17.60	ATOM	1894	CG3	ILE	244	34.008	-1.764	-1.511	1.00	17.60
ATOM	1830	C PRO	236	20.667	-9.112	6.038	1.00	17.60	ATOM	1895	CD1	ILE	244	33.694	-0.698	-2.590	1.00	17.60
ATOM	1831	O PRO	236	21.267	-9.553	7.025	1.00	17.60	ATOM	1896	C	ILE	244	32.150	-3.452	0.301	1.00	17.60
ATOM	1832	N PRO	237	20.583	-9.748	4.860	1.00	17.60	ATOM	1897	O	ILE	244	32.083	-4.406	-0.390	1.00	17.60
ATOM	1833	CD PRO	237	19.949	-9.211	3.665	1.00	17.60	ATOM	1898	N	GLN	245	33.162	-3.448	1.630	1.00	17.60
ATOM	1834	CA PRO	237	21.200	-11.022	6.536	1.00	17.60	ATOM	1899	CA	GLN	245	32.245	-4.681	2.385	1.00	17.60
ATOM	1835	CB PRO	237	20.651	-11.392	3.228	1.00	17.60	ATOM	1900	CB	GLN	245	32.369	-4.238	3.021	1.00	17.60
ATOM	1836	CG PRO	237	19.512	-10.415	2.998	1.00	17.60	ATOM	1901	CG	GLN	245	33.730	-3.611	4.226	1.00	17.60
ATOM	1837	C PRO	237	22.707	-10.963	4.472	1.00	17.60	ATOM	1902	CD	GLN	245	33.687	-2.825	5.540	1.00	17.60
ATOM	1838	O PRO	237	23.426	-11.959	4.649	1.00	17.60	ATOM	1903	CD1	GLN	245	32.855	-2.992	6.430	1.00	17.60
ATOM	1839	N PHE	238	23.063	-9.748	4.045	1.00	17.60	ATOM	1904	NR2	GLN	245	31.599	-1.866	5.626	1.00	17.60
ATOM	1840	CA PHE	238	24.396	-9.244	3.800	1.00	17.60	ATOM	1905	C	GLN	245	31.014	-5.612	2.111	1.00	17.60
ATOM	1841	CB PHE	238	24.708	-8.943	2.331	1.00	17.60	ATOM	1906	O	GLN	245	31.144	-6.823	1.815	1.00	17.60
ATOM	1842	CG PHE	238	24.056	-9.806	1.343	1.00	17.60	ATOM	1907	N	ILE	246	29.904	-4.928	2.086	1.00	17.60
ATOM	1843	CD1 PHE	238	22.085	-9.341	0.831	1.00	17.60	ATOM	1908	CA	ILE	246	28.642	-5.532	1.751	1.00	17.60
ATOM	1844	CD2 PHE	238	26.527	-11.056	1.047	1.00	17.60	ATOM	1909	CB	ILE	246	27.524	-4.441	1.825	1.00	17.60
ATOM	1845	CE1 PHE	238	22.172	-10.362	-0.032	1.00	17.60	ATOM	1910	CG2	ILE	246	26.211	-5.178	1.808	1.00	17.60
ATOM	1846	CE2 PHE	238	23.808	-11.066	0.206	1.00	17.60	ATOM	1911	CG3	ILE	246	27.607	-3.554	3.069	1.00	17.60
ATOM	1847	CE PHE	238	22.630	-11.429	-0.336	1.00	17.60	ATOM	1912	CD1	ILE	246	26.584	-2.427	3.034	1.00	17.60
ATOM	1848	C PHE	238	24.163	-7.086	4.382	1.00	17.60	ATOM	1913	C	ILE	246	28.752	-6.123	0.320	1.00	17.60
ATOM	1849	O PHE	238	23.085	-7.316	4.145	1.00	17.60	ATOM	1914	O	ILE	246	28.544	-7.318	0.014	1.00	17.60
ATOM	1850	N PHE	239	25.228	-7.500	5.099	1.00	17.60	ATOM	1915	N	TYR	247	29.199	-5.272	-0.591	1.00	17.60
ATOM	1851	CA PHE	239	25.462	-6.215	5.740	1.00	17.60	ATOM	1916	CA	TYR	247	29.202	-5.582	-2.014	1.00	17.60
ATOM	1852	CB PHE	239	26.525	-6.033	6.947	1.00	17.60	ATOM	1917	CB	TYR	247	29.089	-6.467	-2.736	1.00	17.60
ATOM	1853	CG PHE	239	24.660	-7.010	6.125	1.00	17.60	ATOM	1918	CG	TYR	247	29.145	-3.139	-2.729	1.00	17.60
ATOM	1854	CD1 PHE	239	26.064	-8.233	8.062	1.00	17.60	ATOM	1919	CD1	TYR	247	29.809	-2.074	-3.269	1.00	17.60
ATOM	1855	CD2 PHE	239	25.398	-6.622	9.225	1.00	17.60	ATOM	1920	CE1	TYR	247	29.199	-0.847	-3.338	1.00	17.60
ATOM	1856	CE1 PHE	239	24.228	-9.107	9.123	1.00	17.60	ATOM	1921	CE2	TYR	247	27.862	-2.998	-2.230	1.00	17.60
ATOM	1857	CE2 PHE	239	25.553	-7.489	10.269	1.00	17.60	ATOM	1922	CE2	TYR	247	27.235	-1.785	-2.379	1.00	17.60
ATOM	1858	C PHE	239	24.972	-8.735	10.228	1.00	17.60	ATOM	1923	CE	TYR	247	27.916	-0.728	-2.846	1.00	17.60
ATOM	1859	G PHE	239	26.956	-6.091	6.193	1.00	17.60	ATOM	1924	ON	TYR	247	27.798	0.476	-3.007	1.00	17.60
ATOM	1860	O PHE	239	27.628	-7.120	6.209	1.00	17.60	ATOM	1925	C	TYR	247	29.866	-6.866	-2.308	1.00	17.60
ATOM	1861	N ALA	240	27.542	-4.889	6.440	1.00	17.60	ATOM	1926	O	TYR	247	29.321	-7.721	-2.981	1.00	17.60
ATOM	1862	CA ALA	240	28.837	-4.616	7.050	1.00	17.60	ATOM	1927	N	GLU	248	30.959	-7.039	-1.620	1.00	17.60
ATOM	1863	CB ALA	240	29.957	-4.786	6.125	1.00	17.60	ATOM	1928	CA	GLU	248	31.782	-8.223	-1.679	1.00	17.60
ATOM	1864	C ALA	240	28.804	-3.127	7.354	1.00	17.60	ATOM	1929	CB	GLU	248	32.844	-8.026	-0.582	1.00	17.60
ATOM	1865	O ALA	240	27.094	-2.518	6.978	1.00	17.60	ATOM	1930	CG	GLU	248	34.007	-9.014	-0.373	1.00	17.60
ATOM	1866	N ASP	241	29.697	-2.372	7.992	1.00	17.60	ATOM	1931	CD	GLU	248	33.591	-10.340	0.283	1.00	17.60
ATOM	1867	CA ASP	241	29.457	-0.922	8.027	1.00	17.60	ATOM	1932	OE1	GLU	248	33.919	-11.422	-0.240	1.00	17.60
ATOM	1868	CB ASP	241	29.698	-0.330	9.428	1.00	17.60	ATOM	1933	OE2	GLU	248	32.922	-10.390	1.328	1.00	17.60
ATOM	1869	CG ASP	241	30.505	-0.130	10.345	1.00	17.60	ATOM	1934	C	GLU	248	30.928	-9.443	-1.494	1.00	17.60
ATOM	1870	OD1 ASP	241	31.687	-1.461	10.058	1.00	17.60	ATOM	1935	O	GLU	248	30.890	-10.306	-2.360	1.00	17.60
ATOM	1871	OD2 ASP	241	29.966	-1.732	11.340	1.00	17.60	ATOM	1936	N	LYS	249	30.157	-9.405	-0.408	1.00	17.60
ATOM	1872	C P	241	30.673	-0.815	7.021	1.00	17.60	ATOM	1937	CA	LYS	249	29.321	-10.511	0.010	1.00	17.60
ATOM	1873	O LSP	241	31.643	-0.535	7.347	1.00	17.60	ATOM	1938	CB	LYS	249	28.797	-10.365	1.433	1.00	17.60
ATOM	1874	N GLN	242	30.121	0.011	5.798	1.00	17.60	ATOM	1939	CG	LYS	249	29.881	-10.314	2.477	1.00	17.60
ATOM	1875	CA GLN	242	31.089	0.687	4.714	1.00	17.60	ATOM	1940	CD	LYS	249	29.981	-9.080	3.367	1.00	17.60
ATOM	1876	CB GLN	242	32.536	0.171	4.787	1.00	17.60	ATOM	1941	CE	LYS	249	28.889	-8.994	4.386	1.00	17.60
ATOM	1877	CG GLN	242	33.588	1.136	5.358	1.00	17.60	ATOM	1942	NE	LYS	249	28.964	-10.140	5.260	1.00	17.60
ATOM	1878	CD GLN	242	33.096	2.089	6.520	1.00	17.60	ATOM	1943	C	LYS	249	28.134	-10.775	-0.802	1.00	17.60
ATOM	1879	OE1 GLN	242	32.384	3.002	6.315	1.00	17.60	ATOM	1944	O	LYS	249	27.635	-11.889	-0.901	1.00	17.60
ATOM	1880	NE2 GLN	242	33.411	1.676	7.772	1.00	17.60	ATOM	1945	N	ILE	250	27.640	-9.645	-1.300	1.00	17.60
ATOM	1881	C GLN	242	30.563	-0.337	3.542	1.00	17.60	ATOM	1946	CA	ILE	250	26.441	-9.590	-2.113	1.00	17.60
ATOM	1882	O GLN	242	30.838	-1.547	3.494	1.00	17.60	ATOM	1947	CB	ILE	250	26.178	-8.092	-2.359	1.00	17.60



ATOM	1910	CG1 ILE	250	25.909	-7.738	-3.010	1.00	17.60	ATOM	2013	C	PRO	258	10.080	-19.017	11.104	1.00	17.60	
ATOM	1919	CG1 ILE	250	26.990	-7.710	-1.462	1.00	17.60	ATOM	2014	O	PRO	258	17.476	-20.464	10.310	1.00	17.60	
ATOM	1950	CD1 ILE	250	23.529	-7.031	-1.968	1.00	17.60	ATOM	2015	N	SER	259	10.244	-20.223	12.430	1.00	17.60	
ATOM	1951	C	ILE	250	26.014	-10.405	-3.321	1.00	17.60	ATOM	2016	CA	SER	259	17.652	-21.470	12.911	1.00	17.60
ATOM	1952	O	ILE	250	26.155	-11.384	-3.663	1.00	17.60	ATOM	2017	CB	SER	259	10.197	-21.803	14.309	1.00	17.60
ATOM	1953	N	VAL	251	27.991	-10.077	-3.835	1.00	17.60	ATOM	2018	OS	SER	259	10.408	-20.589	15.064	1.00	17.60
ATOM	1954	CA	VAL	251	20.492	-10.717	-5.003	1.00	17.60	ATOM	2019	C	SER	259	16.129	-21.414	12.586	1.00	17.60
ATOM	1955	CB	VAL	251	29.633	-9.012	-5.416	1.00	17.60	ATOM	2020	O	SER	259	15.476	-22.451	12.091	1.00	17.60
ATOM	1956	CG1 VAL	251	30.539	-10.426	-6.423	1.00	17.60	ATOM	2021	N	HIS	260	15.524	-20.217	13.135	1.00	17.60	
ATOM	1957	CG2 VAL	251	29.038	-8.669	-6.202	1.00	17.60	ATOM	2022	CA	HIS	260	14.070	-20.105	13.298	1.00	17.60	
ATOM	1958	C	VAL	251	28.033	-12.173	-4.762	1.00	17.60	ATOM	2023	CB	HIS	260	13.732	-18.943	14.251	1.00	17.60
ATOM	1959	O	VAL	251	28.519	-12.956	-5.651	1.00	17.60	ATOM	2024	CC	HIS	260	14.151	-17.562	13.011	1.00	17.60
ATOM	1960	N	SER	252	29.309	-12.601	-3.638	1.00	17.60	ATOM	2025	CD2 HIS	260	15.467	-17.094	13.752	1.00	17.60	
ATOM	1961	CA	SER	252	29.765	-14.070	-3.692	1.00	17.60	ATOM	2026	ND1 HIS	260	13.362	-16.566	13.455	1.00	17.60	
ATOM	1962	CB	SER	252	30.662	-16.234	-2.308	1.00	17.60	ATOM	2027	CE1 HIS	260	14.109	-15.511	13.109	1.00	17.60	
ATOM	1963	CG	SER	252	30.253	-13.510	-1.147	1.00	17.60	ATOM	2028	NE2 HIS	260	15.371	-15.014	13.373	1.00	17.60	
ATOM	1964	C	SER	252	20.571	-14.081	-3.317	1.00	17.60	ATOM	2029	C	HIS	260	13.271	-19.916	12.003	1.00	17.60
ATOM	1965	O	SER	252	28.509	-15.946	-3.916	1.00	17.60	ATOM	2030	O	HIS	260	12.101	-19.314	12.000	1.00	17.60
ATOM	1966	N	GLY	253	27.639	-14.472	-2.469	1.00	17.60	ATOM	2031	X	PHE	261	13.036	-20.427	10.901	1.00	17.60
ATOM	1967	CA	GLY	253	26.388	-15.217	-2.417	1.00	17.60	ATOM	2032	CA	PHE	261	13.273	-20.100	9.641	1.00	17.60
ATOM	1968	C	GLY	253	26.565	-16.642	-1.094	1.00	17.60	ATOM	2033	CB	PHE	261	14.396	-19.027	0.707	1.00	17.60
ATOM	1969	O	GLY	253	26.746	-17.690	-2.502	1.00	17.60	ATOM	2034	CG	PHE	261	14.538	-18.327	0.566	1.00	17.60
ATOM	1970	N	LYS	254	26.606	-16.541	-0.599	1.00	17.60	ATOM	2035	CD1 PHE	261	13.971	-17.432	9.495	1.00	17.60	
ATOM	1971	CA	LYS	254	26.495	-17.657	0.295	1.00	17.60	ATOM	2036	CD2 PHE	261	15.254	-17.012	7.400	1.00	17.60	
ATOM	1972	CB	LYS	254	27.782	-17.007	1.041	1.00	17.60	ATOM	2037	CB1 PHE	261	14.127	-16.067	9.347	1.00	17.60	
ATOM	1973	CG	LYS	254	28.099	-17.900	0.081	1.00	17.60	ATOM	2038	CE2 PHE	261	15.403	-16.446	7.349	1.00	17.60	
ATOM	1974	CD	LYS	254	30.174	-18.310	0.000	1.00	17.60	ATOM	2039	CB	PHE	261	14.002	-15.578	0.773	1.00	17.60
ATOM	1975	CE	LYS	254	31.293	-18.116	-0.230	1.00	17.60	ATOM	2040	C	PHE	261	12.285	-21.005	9.003	1.00	17.60
ATOM	1976	N2	LYS	254	31.131	-18.971	-1.459	1.00	17.60	ATOM	2041	O	PHE	261	11.400	-20.459	0.362	1.00	17.60
ATOM	1977	C	LYS	254	25.433	-16.953	1.142	1.00	17.60	ATOM	2042	N	SER	262	12.265	-22.302	9.171	1.00	17.60
ATOM	1978	O	LYS	254	25.746	-15.010	1.500	1.00	17.60	ATOM	2043	CA	SER	262	11.352	-23.169	0.427	1.00	17.60
ATOM	1979	N	VAL	255	24.201	-17.354	1.402	1.00	17.60	ATOM	2044	CB	SER	262	9.090	-22.602	0.169	1.00	17.60
ATOM	1980	CA	VAL	255	23.342	-16.510	2.349	1.00	17.60	ATOM	2045	CG	SER	262	9.666	-21.938	0.986	1.00	17.60
ATOM	1981	CB	VAL	255	21.033	-16.360	1.096	1.00	17.60	ATOM	2046	C	SER	262	11.955	-23.265	7.043	1.00	17.60
ATOM	1982	CG1 VAL	255	21.370	-15.030	2.470	1.00	17.60	ATOM	2047	O	SER	262	12.596	-22.333	6.503	1.00	17.60	
ATOM	1983	CG2 VAL	255	21.603	-16.482	0.380	1.00	17.60	ATOM	2048	N	SER	263	11.723	-24.469	6.494	1.00	17.60	
ATOM	1984	C	VAL	255	21.328	-17.306	3.654	1.00	17.60	ATOM	2049	CA	SER	263	12.283	-24.032	5.191	1.00	17.60
ATOM	1985	O	VAL	255	23.611	-18.524	3.500	1.00	17.60	ATOM	2050	CB	SER	263	11.097	-26.302	4.915	1.00	17.60
ATOM	1986	N	ARG	256	22.972	-16.756	4.044	1.00	17.60	ATOM	2051	CG	SER	263	12.062	-27.159	6.008	1.00	17.60
ATOM	1987	CA	ARG	256	22.922	-17.560	.063	1.00	17.60	ATOM	2052	C	SER	263	11.727	-23.060	4.163	1.00	17.60
ATOM	1988	CB	ARG	256	24.105	-17.351	.090	1.00	17.60	ATOM	2053	O	SER	263	12.470	-23.119	3.535	1.00	17.60
ATOM	1989	CG	ARG	256	25.219	-18.002	.447	1.00	17.60	ATOM	2054	N	ASP	264	10.411	-23.700	4.267	1.00	17.60
ATOM	1990	CD	ARG	256	24.903	-19.535	6.067	1.00	17.60	ATOM	2055	CA	ASP	264	9.639	-22.927	3.318	1.00	17.60
ATOM	1991	NE	ARG	256	25.622	-20.115	0.025	1.00	17.60	ATOM	2056	CB	ASP	264	0.211	-22.772	3.051	1.00	17.60
ATOM	1992	CE	ARG	256	26.514	-19.551	0.060	1.00	17.60	ATOM	2057	CG	ASP	264	7.203	-23.000	3.522	1.00	17.60
ATOM	1993	NH1 ARG	256	26.014	-18.263	0.015	1.00	17.60	ATOM	2058	OD1 ASP	264	6.083	-23.650	3.977	1.00	17.60		
ATOM	1994	NH2 ARG	256	27.050	-20.395	9.000	1.00	17.60	ATOM	2059	OD2 ASP	264	7.402	-24.909	2.057	1.00	17.60		
ATOM	1995	C	ARG	256	21.660	-17.605	6.910	1.00	17.60	ATOM	2060	C	ASP	264	10.214	-21.573	3.004	1.00	17.60
ATOM	1996	O	ARG	256	21.452	-16.912	7.098	1.00	17.60	ATOM	2061	O	ASP	264	10.463	-21.290	1.017	1.00	17.60
ATOM	1997	N	PHE	257	20.016	-16.510	6.545	1.00	17.6										

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ATOM	2078	O	LYS	266	15.661	-20.402	1.241	1.00	17.60	20.062	-10.311	-9.291	1.00	17.60
ATOM	2079	N	ASP	267	13.601	-21.654	1.618	1.00	17.60	21.058	-19.500	-7.401	1.00	17.60
ATOM	2080	CA	ASP	267	13.439	-22.100	0.291	1.00	17.60	20.747	-15.696	-7.423	1.00	17.60
ATOM	2081	CB	ASP	267	12.412	-23.146	0.244	1.00	17.60	20.352	-16.512	-7.048	1.00	17.60
ATOM	2082	CG	ASP	267	12.441	-23.703	-1.155	1.00	17.60	21.973	-16.060	-7.758	1.00	17.60
ATOM	2083	CD	ASP	267	13.479	-24.264	-1.538	1.00	17.60	22.941	-15.123	-6.329	1.00	17.60
ATOM	2084	OD1	ASP	267	11.453	-23.513	-1.869	1.00	17.60	24.315	-15.698	-6.033	1.00	17.60
ATOM	2085	OD2	ASP	267	13.018	-20.983	-0.607	1.00	17.60	25.404	-16.783	-6.570	1.00	17.60
ATOM	2086	O	ASP	267	13.476	-20.936	-1.756	1.00	17.60	24.499	-15.803	-6.540	1.00	17.60
ATOM	2087	N	LEU	268	12.135	-20.084	-0.212	1.00	17.60	22.764	-16.832	-9.018	1.00	17.60
ATOM	2088	CA	LEU	268	11.825	-19.036	-1.164	1.00	17.60	23.037	-13.758	-10.410	1.00	17.60
ATOM	2089	CB	LEU	268	10.565	-18.374	-0.662	1.00	17.60	22.308	-15.958	-10.354	1.00	17.60
ATOM	2090	CG	LEU	268	9.929	-17.186	-1.362	1.00	17.60	22.149	-16.146	-11.764	1.00	17.60
ATOM	2091	CD1	LEU	269	9.629	-17.167	-2.039	1.00	17.60	22.674	-17.635	-11.990	1.00	17.60
ATOM	2092	CD2	LEU	268	8.717	-16.925	-0.465	1.00	17.60	22.686	-18.328	-13.434	1.00	17.60
ATOM	2093	C	LEU	268	13.415	-17.603	-2.339	1.00	17.60	22.649	-19.360	-13.653	1.00	17.60
ATOM	2094	O	LEU	268	13.740	-17.927	-0.174	1.00	17.60	22.913	-17.260	-14.316	1.00	17.60
ATOM	2095	N	LEU	269	14.897	-17.062	-0.147	1.00	17.60	20.771	-15.751	-12.262	1.00	17.60
ATOM	2096	CA	LEU	269	15.249	-16.867	1.312	1.00	17.60	19.813	-16.508	-12.101	1.00	17.60
ATOM	2097	CB	LEU	269	14.508	-15.807	2.099	1.00	17.60	20.644	-14.624	-12.931	1.00	17.60
ATOM	2098	CG	LEU	269	13.094	-15.659	1.679	1.00	17.60	19.377	-14.232	-13.555	1.00	17.60
ATOM	2099	CH1	LEU	269	14.562	-16.213	3.540	1.00	17.60	19.595	-13.082	-16.556	1.00	17.60
ATOM	2100	CD1	LEU	269	16.078	-17.569	-0.966	1.00	17.60	19.963	-11.735	-13.917	1.00	17.60
ATOM	2101	C	LEU	269	16.692	-16.845	-1.750	1.00	17.60	19.660	-10.451	-16.766	1.00	17.60
ATOM	2102	O	LEU	269	16.330	-18.847	-0.079	1.00	17.60	19.057	-11.628	-12.717	1.00	17.60
ATOM	2103	N	ARG	270	17.451	-19.804	-3.586	1.00	17.60	18.376	-15.303	-16.270	1.00	17.60
ATOM	2104	CA	ARG	270	17.755	-20.782	-3.029	1.00	17.60	17.359	-15.665	-14.130	1.00	17.60
ATOM	2105	CB	ARG	270	16.508	-21.696	-3.282	1.00	17.60	19.276	-16.134	-14.987	1.00	17.60
ATOM	2106	CG	ARG	270	16.759	-21.140	-0.894	1.00	17.60	18.372	-17.243	-15.617	1.00	17.60
ATOM	2107	CD	ARG	270	16.966	-23.257	0.549	1.00	17.60	19.543	-17.883	-16.527	1.00	17.60
ATOM	2108	NE	ARG	270	17.099	-24.451	1.196	1.00	17.60	20.167	-16.780	-17.326	1.00	17.60
ATOM	2109	CE	ARG	270	17.087	-25.644	0.538	1.00	17.60	19.095	-19.080	-17.353	1.00	17.60
ATOM	2110	NH1	ARG	270	17.287	-26.439	2.536	1.00	17.60	17.859	-18.249	-14.695	1.00	17.60
ATOM	2111	NH2	ARG	270	17.082	-19.465	-3.058	1.00	17.60	16.909	-18.985	-15.117	1.00	17.60
ATOM	2112	C	ARG	270	17.967	-19.643	-3.090	1.00	17.60	18.262	-18.427	-13.447	1.00	17.60
ATOM	2113	O	ASN	271	15.795	-19.377	-3.415	1.00	17.60	17.528	-19.292	-12.534	1.00	17.60
ATOM	2114	N	ASN	271	15.368	-19.268	-4.813	1.00	17.60	18.534	-20.258	-12.048	1.00	17.60
ATOM	2115	CA	ASN	271	13.997	-19.901	-5.159	1.00	17.60	19.377	-20.905	-13.147	1.00	17.60
ATOM	2116	CB	ASN	271	13.780	-21.417	-3.78	1.00	17.60	20.538	-21.679	-12.474	1.00	17.60
ATOM	2117	CG	ASN	271	12.743	-21.913	-8.07	1.00	17.60	20.130	-22.739	-13.426	1.00	17.60
ATOM	2118	OD1	ASN	271	14.614	-22.258	-5.926	1.00	17.60	21.325	-23.429	-10.933	1.00	17.60
ATOM	2119	ND2	ASN	271	15.173	-17.803	-5.208	1.00	17.60	16.790	-18.583	-11.351	1.00	17.60
ATOM	2120	C	ASN	271	14.920	-17.565	-6.389	1.00	17.60	16.134	-19.212	-10.510	1.00	17.60
ATOM	2121	O	ASN	271	15.160	-16.770	-4.362	1.00	17.60	16.923	-17.212	-11.253	1.00	17.60
ATOM	2122	N	LEU	272	15.026	-15.417	-4.879	1.00	17.60	16.230	-16.426	-10.266	1.00	17.60
ATOM	2123	CA	LEU	272	14.030	-14.590	-4.070	1.00	17.60	16.431	-16.988	-10.571	1.00	17.60
ATOM	2124	CB	LEU	272	12.524	-14.755	-4.354	1.00	17.60	16.030	-16.078	-9.408	1.00	17.60
ATOM	2125	CG	LEU	272	11.600	-16.164	-3.288	1.00	17.60	16.787	-12.717	-9.345	1.00	17.60
ATOM	2126	CD1	LEU	272	12.314	-16.077	-5.697	1.00	17.60	18.231	-12.942	-9.196	1.00	17.60
ATOM	2127	CD2	LEU	272	16.369	-16.767	-4.814	1.00	17.60	19.132	-11.916	-9.404	1.00	17.60
ATOM	2128	C	LEU	272	16.756	-14.083	-5.736	1.00	17.60	18.697	-10.723	-9.742	1.00	17.60
ATOM	2129	O	LEU	272	17.150	-14.997	-3.789	1.00	17.60	20.631	-12.182	-9.353	1.00	17.60
ATOM	2130	N	LEU	273	18.478	-14.433	-3.662	1.00	17.60	14.719	-16.649	-10.208	1.00	17.60
ATOM	2131	CA	LEU	273	18.712	-14.301	-2.191	1.00	17.60	14.064	-16.601	-11.265	1.00	17.60
ATOM	2132	CB	LEU	273	18.081	-13.074	-1.609	1.00	17.60	14.094	-16.867	-9.040	1.00	17.60
ATOM	2133	CG	LEU	273	17.460	-13.322	-0.284	1.00	17.60	12.646	-16.973	-9.000	1.00	17.60
ATOM	2134	CD1	LEU	273	19.166	-12.083	-1.404	1.00	17.60	12.104	-17.199	-7.650	1.00	17.60
ATOM	2135	CD2	LEU	273	19.486	-15.317	-4.365	1.00	17.60	11.552	-18.593	-7.423	1.00	17.60
ATOM	2136	C	LEU	273	20.508	-15.807	-3.843	1.00	17.60	12.056	-19.689	-8.102	1.00	17.60
ATOM	2137	O	LEU	273	19.128	-15.468	-5.652	1.00	17.60	10.514	-18.743	-6.518	1.00	17.60
ATOM	2138	N	GLN	274	19.727	-16.398	-6.619	1.00	17.60	11.507	-20.926	-7.866	1.00	17.60
ATOM	2139	CA	GLN	274	18.642	-16.958	-7.577	1.00	17.60	9.963	-19.972	-6.283	1.00	17.60
ATOM	2140	CB	GLN	274	18.856	-18.439	-8.016	1.00	17.60	10.461	-21.054	-6.961	1.00	17.60
ATOM	2141	CG	GLN	274	20.301	-18.797	-8.317	1.00	17.60	12.114	-15.639	-9.416	1.00	17.60
ATOM	2142	CD	GLN	274						12.663	-14.671	-9.018	1.00	17.60



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ATOM	2208	N	GLY	202	11.101	-15.577	-10.240	1.00	17.60	6.474	-16.512	-6.425	1.00	17.60
ATOM	2209	CA	GLY	202	10.607	-14.291	-10.639	1.00	17.60	6.661	-14.970	-6.302	1.00	17.60
ATOM	2210	C	GLY	202	11.271	-13.972	-11.972	1.00	17.60	6.664	-14.635	-4.029	1.00	17.60
ATOM	2211	O	GLY	202	10.756	-13.048	-12.640	1.00	17.60	6.052	-14.467	-6.694	1.00	17.60
ATOM	2212	N	ASN	203	12.248	-16.665	-12.445	1.00	17.60	6.564	-14.549	-8.022	1.00	17.60
ATOM	2213	CA	ASN	203	12.743	-16.346	-13.787	1.00	17.60	5.173	-16.889	-5.783	1.00	17.60
ATOM	2214	CR	ASN	203	14.253	-14.225	-13.769	1.00	17.60	5.173	-17.600	-4.701	1.00	17.60
ATOM	2215	CG	ASN	203	14.726	-13.157	-16.756	1.00	17.60	4.067	-16.535	-6.407	1.00	17.60
ATOM	2216	OD1	ASN	203	15.915	-12.830	-14.738	1.00	17.60	2.714	-16.893	-5.911	1.00	17.60
ATOM	2217	ND2	ASN	203	13.941	-12.500	-15.629	1.00	17.60	1.584	-16.437	-6.896	1.00	17.60
ATOM	2218	C	ASN	203	12.381	-15.324	-14.908	1.00	17.60	1.650	-14.895	-7.147	1.00	17.60
ATOM	2219	O	ASN	203	12.862	-15.015	-16.080	1.00	17.60	0.355	-14.500	-8.307	1.00	17.60
ATOM	2220	N	LEU	204	11.932	-16.517	-14.517	1.00	17.60	0.312	-13.032	-8.233	1.00	17.60
ATOM	2221	CA	LEU	204	11.710	-17.686	-15.303	1.00	17.60	-0.907	-12.702	-8.936	1.00	17.60
ATOM	2222	CB	LEU	204	11.626	-18.940	-14.491	1.00	17.60	2.428	-10.376	-5.617	1.00	17.60
ATOM	2223	CO	LEU	204	12.476	-18.906	-13.225	1.00	17.60	1.608	-10.632	-6.701	1.00	17.60
ATOM	2224	CD1	LEU	204	11.020	-19.839	-12.251	1.00	17.60	3.021	-19.398	-6.228	1.00	17.60
ATOM	2225	CD2	LEU	204	13.929	-19.198	-13.510	1.00	17.60	2.531	-20.742	-5.988	1.00	17.60
ATOM	2226	C	LEU	204	10.419	-17.549	-16.224	1.00	17.60	2.510	-21.531	-7.291	1.00	17.60
ATOM	2227	O	LEU	204	9.615	-16.696	-15.871	1.00	17.60	1.479	-20.958	-8.248	1.00	17.60
ATOM	2228	N	LYS	205	10.230	-18.339	-17.305	1.00	17.60	0.486	-20.383	-7.817	1.00	17.60
ATOM	2229	CA	LYS	205	8.936	-18.322	-18.055	1.00	17.60	3.425	-21.411	-4.998	1.00	17.60
ATOM	2230	CB	LYS	205	8.971	-19.381	-19.222	1.00	17.60	3.142	-22.630	-4.822	1.00	17.60
ATOM	2231	CO	LYS	205	10.215	-19.010	-20.105	1.00	17.60	5.265	-21.176	-3.527	1.00	17.60
ATOM	2232	CD	LYS	205	10.130	-19.097	-21.638	1.00	17.60	6.272	-20.255	-3.053	1.00	17.60
ATOM	2233	CE	LYS	205	11.372	-18.332	-22.220	1.00	17.60	7.522	-20.993	-2.634	1.00	17.60
ATOM	2234	NE	LYS	205	11.437	-18.246	-23.694	1.00	17.60	8.578	-21.241	-3.477	1.00	17.60
ATOM	2235	C	LYS	205	7.899	-18.680	-16.999	1.00	17.60	7.909	-21.326	-1.380	1.00	17.60
ATOM	2236	O	LYS	205	8.161	-19.657	-16.328	1.00	17.60	9.162	-21.724	-1.491	1.00	17.60
ATOM	2237	N	ASP	206	6.873	-17.889	-16.725	1.00	17.60	9.364	-21.675	-2.745	1.00	17.60
ATOM	2238	CA	ASP	206	5.878	-17.968	-15.610	1.00	17.60	4.359	-21.590	-2.337	1.00	17.60
ATOM	2239	CB	ASP	206	6.063	-19.163	-14.595	1.00	17.60	3.915	-20.876	-2.707	1.00	17.60
ATOM	2240	CC	ASP	206	5.723	-20.638	-15.087	1.00	17.60	3.100	-22.737	-2.049	1.00	17.60
ATOM	2241	OD1	ASP	206	4.767	-20.877	-15.812	1.00	17.60	4.737	-23.486	-0.880	1.00	17.60
ATOM	2242	OD2	ASP	206	6.375	-21.549	-14.746	1.00	17.60	5.771	-24.624	-0.775	1.00	17.60
ATOM	2243	C	ASP	206	6.234	-16.620	-14.950	1.00	17.60	6.025	-25.636	-3.993	1.00	17.60
ATOM	2244	O	ASP	206	5.837	-15.511	-15.415	1.00	17.60	6.683	-25.162	-3.393	1.00	17.60
ATOM	2245	N	GLY	207	7.004	-16.550	-13.886	1.00	17.60	0.166	-24.629	-3.400	1.00	17.60
ATOM	2246	CA	GLY	207	7.401	-15.215	-13.364	1.00	17.60	0.662	-24.062	-4.677	1.00	17.60
ATOM	2247	C	GLY	207	7.755	-15.095	-12.039	1.00	17.60	4.682	-22.556	0.338	1.00	17.60
ATOM	2248	O	GLY	207	7.018	-15.079	-11.132	1.00	17.60	3.745	-22.673	1.107	1.00	17.60
ATOM	2249	N	VAL	208	5.847	-14.136	-11.946	1.00	17.60	5.530	-21.520	0.456	1.00	17.60
ATOM	2250	CA	VAL	208	5.110	-13.879	-10.718	1.00	17.60	5.439	-20.578	1.581	1.00	17.60
ATOM	2251	CB	VAL	208	3.916	-12.973	-10.820	1.00	17.60	6.886	-19.688	1.585	1.00	17.60
ATOM	2252	CG1	VAL	208	6.073	-12.101	-9.566	1.00	17.60	6.964	-18.046	2.840	1.00	17.60
ATOM	2253	CG2	VAL	208	3.966	-12.148	-12.093	1.00	17.60	6.771	-17.488	3.002	1.00	17.60
ATOM	2254	C	VAL	208	4.417	-15.140	-10.221	1.00	17.60	7.198	-17.488	3.002	1.00	17.60
ATOM	2255	O	VAL	208	4.450	-15.119	-9.024	1.00	17.60	6.314	-16.431	2.248	1.00	17.60
ATOM	2256	N	ASN	209	3.825	-15.994	-11.059	1.00	17.60	7.484	-19.413	3.984	1.00	17.60
ATOM	2257	CA	ASN	209	3.190	-17.197	-10.541	1.00	17.60	7.614	-18.430	4.866	1.00	17.60
ATOM	2258	CB	ASN	209	2.306	-17.880	-11.598	1.00	17.60	7.187	-16.013	4.937	1.00	17.60
ATOM	2259	CG	ASN	209	1.085	-16.978	-11.756	1.00	17.60	6.307	-15.193	2.850	1.00	17.60
ATOM	2260	OD1	ASN	209	1.126	-16.013	-12.526	1.00	17.60	6.737	-14.995	4.163	1.00	17.60
ATOM	2261	ND2	ASN	209	0.080	-17.132	-10.992	1.00	17.60	4.165	-19.701	1.506	1.00	17.60
ATOM	2262	C	ASN	209	4.174	-18.204	-10.012	1.00	17.60	3.579	-19.452	2.552	1.00	17.60
ATOM	2263	O	ASN	209	3.734	-19.257	-9.588	1.00	17.60	3.657	-19.184	0.394	1.00	17.60
ATOM	2264	N	ASP	210	5.486	-17.972	-9.994	1.00	17.60	2.487	-18.343	0.457	1.00	17.60
ATOM	2265	CA	ASP	210	6.383	-18.905	-9.364	1.00	17.60	2.293	-17.272	-0.617	1.00	17.60
ATOM	2266	CB	ASP	210	7.806	-18.803	-9.886	1.00	17.60	3.354	-16.198	-0.817	1.00	17.60
ATOM	2267	CC	ASP	210	8.101	-19.139	-11.359	1.00	17.60	3.212	-14.984	-0.219	1.00	17.60
ATOM	2268	OD1	ASP	210	8.797	-18.348	-12.028	1.00	17.60	4.647	-16.437	-2.616	1.00	17.60
ATOM	2269	OD2	ASP	210	7.687	-20.204	-11.835	1.00	17.60	4.153	-13.998	-0.408	1.00	17.60
ATOM	2270	C	P	210	6.124	-18.357	-7.955	1.00	17.60	5.385	-15.447	-1.708	1.00	17.60
ATOM	2271	O	ASP	210	6.118	-19.151	-7.028	1.00	17.60					
ATOM	2272	N	ILE	211	6.487	-17.022	-7.767	1.00	17.60					

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ATOM	2338	CE	PHE	297	5.246	-14.227	-3.198	1.00	17.60	ATOM	2403	N	TYR	306	-5.549	-9.194	-2.285	1.00	17.60
ATOM	2339	C	PHE	297	1.536	-19.393	0.061	1.00	17.60	ATOM	2404	CA	TYR	306	-5.746	-7.123	-3.203	1.00	17.60
ATOM	2340	O	PHE	297	1.583	-19.026	-1.092	1.00	17.60	ATOM	2405	CB	TYR	306	-5.939	-7.753	-4.563	1.00	17.60
ATOM	2341	N	ALA	298	-0.713	-19.049	0.981	1.00	17.60	ATOM	2406	CG	TYR	306	-6.361	-6.686	-5.574	1.00	17.60
ATOM	2342	CA	ALA	298	-0.275	-20.041	0.574	1.00	17.60	ATOM	2407	CD1	TYR	306	-7.669	-6.581	-6.010	1.00	17.60
ATOM	2343	CB	ALA	298	0.378	-22.228	0.736	1.00	17.60	ATOM	2408	CP1	TYR	306	-8.075	-5.493	-6.812	1.00	17.60
ATOM	2344	C	ALA	298	-1.622	-20.745	1.320	1.00	17.60	ATOM	2409	CP2	TYR	306	-5.427	-5.776	-5.897	1.00	17.60
ATOM	2345	O	ALA	298	-2.685	-21.258	0.927	1.00	17.60	ATOM	2410	CE2	TYR	306	-5.829	-6.660	-6.662	1.00	17.60
ATOM	2346	N	THR	299	-1.579	-20.026	2.426	1.00	17.60	ATOM	2411	CE1	TYR	306	-7.134	-6.532	-7.110	1.00	17.60
ATOM	2347	CA	THR	299	-2.622	-19.500	3.219	1.00	17.60	ATOM	2412	CH	TYR	306	-7.490	-3.393	-7.021	1.00	17.60
ATOM	2348	CB	THR	299	-2.353	-19.417	4.667	1.00	17.60	ATOM	2413	C	TYR	306	-6.889	-6.222	-7.785	1.00	17.60
ATOM	2349	CG1	THR	299	-0.716	-19.680	4.730	1.00	17.60	ATOM	2414	O	TYR	306	-6.786	-6.993	-3.811	1.00	17.60
ATOM	2350	CG2	THR	299	-3.061	-20.284	5.495	1.00	17.60	ATOM	2415	N	GLN	307	-7.986	-6.799	-2.301	1.00	17.60
ATOM	2351	C	THR	299	-2.938	-18.052	2.701	1.00	17.60	ATOM	2416	CA	GLN	307	-9.195	-6.015	-1.971	1.00	17.60
ATOM	2352	O	THR	299	-3.738	-17.286	3.304	1.00	17.60	ATOM	2417	CB	GLN	307	-10.433	-6.917	-1.053	1.00	17.60
ATOM	2353	N	THR	300	-2.700	-17.633	1.633	1.00	17.60	ATOM	2418	CD	GLN	307	-11.143	-7.406	-3.166	1.00	17.60
ATOM	2354	CA	THR	300	-2.331	-16.313	1.070	1.00	17.60	ATOM	2419	CD	GLN	307	-11.813	-8.816	-3.125	1.00	17.60
ATOM	2355	CB	THR	300	-0.990	-15.359	0.461	1.00	17.60	ATOM	2420	OE1	GLN	307	-12.418	-9.302	-2.132	1.00	17.60
ATOM	2356	CG1	THR	300	-0.035	-16.067	1.459	1.00	17.60	ATOM	2421	NE2	GLN	307	-11.727	-9.563	-4.248	1.00	17.60
ATOM	2357	CG2	THR	300	-1.017	-14.548	-0.057	1.00	17.60	ATOM	2422	C	GLN	307	-9.066	-5.261	-0.656	1.00	17.60
ATOM	2358	C	THR	300	-3.459	-16.304	0.058	1.00	17.60	ATOM	2423	D	GLN	307	-10.066	-4.709	-0.122	1.00	17.60
ATOM	2359	O	THR	300	-3.424	-17.025	-0.923	1.00	17.60	ATOM	2424	N	ARG	308	-7.016	-5.279	-0.166	1.00	17.60
ATOM	2360	N	ASP	301	-4.539	-15.576	0.305	1.00	17.60	ATOM	2425	CA	ARG	308	-7.375	-4.763	1.324	1.00	17.60
ATOM	2361	CA	ASP	301	-5.601	-15.432	-0.643	1.00	17.60	ATOM	2426	CB	ARG	308	-7.596	-3.275	1.396	1.00	17.60
ATOM	2362	CB	ASP	301	-6.967	-15.559	0.035	1.00	17.60	ATOM	2427	CG	ARG	308	-6.628	-2.628	0.084	1.00	17.60
ATOM	2363	CG	ASP	301	-8.371	-15.665	-0.895	1.00	17.60	ATOM	2428	CD	ARG	308	-7.336	-1.203	0.288	1.00	17.60
ATOM	2364	OD1	ASP	301	-9.276	-15.948	-0.385	1.00	17.60	ATOM	2429	NE	ARG	308	-6.016	-0.516	0.078	1.00	17.60
ATOM	2365	OD2	ASP	301	-8.041	-15.398	-2.116	1.00	17.60	ATOM	2430	CE	ARG	308	-5.972	-0.300	2.183	1.00	17.60
ATOM	2366	C	ASP	301	-5.370	-16.030	-1.192	1.00	17.60	ATOM	2431	NH1	ARG	308	-6.952	-0.752	3.002	1.00	17.60
ATOM	2367	O	ASP	301	-5.737	-12.941	-0.684	1.00	17.60	ATOM	2432	NH2	ARG	308	-5.004	0.524	2.615	1.00	17.60
ATOM	2368	N	TRP	302	-4.732	-14.165	-2.331	1.00	17.60	ATOM	2433	C	ARG	308	-8.278	-5.502	2.045	1.00	17.60
ATOM	2369	CA	TRP	302	-4.237	-13.050	-3.081	1.00	17.60	ATOM	2434	O	ARG	308	-8.570	-6.670	1.800	1.00	17.60
ATOM	2370	CB	TRP	302	-3.619	-13.588	-0.289	1.00	17.60	ATOM	2435	N	LYS	309	-8.667	-8.056	3.121	1.00	17.60
ATOM	2371	CG	TRP	302	-2.353	-14.329	-0.840	1.00	17.60	ATOM	2436	CA	LYS	309	-9.689	-5.356	4.021	1.00	17.60
ATOM	2372	CD2	TRP	302	-1.097	-13.821	-3.714	1.00	17.60	ATOM	2437	CB	LYS	309	-11.135	-5.108	3.338	1.00	17.60
ATOM	2373	CE2	TRP	302	-0.317	-14.976	-3.721	1.00	17.60	ATOM	2438	CG	LYS	309	-11.535	-3.759	2.568	1.00	17.60
ATOM	2374	CE3	TRP	302	-0.454	-12.649	-3.429	1.00	17.60	ATOM	2439	CD	LYS	309	-12.024	-2.488	3.363	1.00	17.60
ATOM	2375	CD1	TRP	302	-2.356	-15.678	-4.216	1.00	17.60	ATOM	2440	CE	LYS	309	-11.843	-1.024	2.763	1.00	17.60
ATOM	2376	NE1	TRP	302	-1.099	-16.041	-4.013	1.00	17.60	ATOM	2441	NE	LYS	309	-12.705	-0.667	1.625	1.00	17.60
ATOM	2377	CE2	TRP	302	1.050	-14.961	-3.658	1.00	17.60	ATOM	2442	C	LYS	309	-9.481	-6.846	4.410	1.00	17.60
ATOM	2378	CE3	TRP	302	0.900	-12.610	-3.170	1.00	17.60	ATOM	2443	O	LYS	309	-8.782	-7.197	5.383	1.00	17.60
ATOM	2379	CH2	TRP	302	1.660	-13.769	-3.182	1.00	17.60	ATOM	2444	N	VAL	310	-9.956	-7.716	3.522	1.00	17.60
ATOM	2380	C	TRP	302	-5.367	-12.097	-3.382	1.00	17.60	ATOM	2445	CA	VAL	310	-10.080	-9.134	3.772	1.00	17.60
ATOM	2381	O	TRP	302	-5.162	-10.909	-3.183	1.00	17.60	ATOM	2446	CB	VAL	310	-10.474	-9.846	2.386	1.00	17.60
ATOM	2382	N	ILE	303	-6.599	-12.471	-3.721	1.00	17.60	ATOM	2447	CG1	VAL	310	-11.106	-11.205	2.768	1.00	17.60
ATOM	2383	CA	ILE	303	-7.576	-11.396	-3.977	1.00	17.60	ATOM	2448	CG2	VAL	310	-11.537	-9.078	1.524	1.00	17.60
ATOM	2384	CB	ILE	303	-8.794	-11.859	-4.852	1.00	17.60	ATOM	2449	C	VAL	310	-8.859	-9.765	4.443	1.00	17.60
ATOM	2385	CG2	ILE	303	-8.121	-12.842	-6.004	1.00	17.60	ATOM	2450	O	VAL	310	-9.125	-10.620	5.459	1.00	17.60
ATOM	2386	CG1	ILE	303	-9.881	-12.679	-4.128	1.00	17.60	ATOM	2451	N	GLU	311	-7.567	-9.615	6.075	1.00	17.60
ATOM	2387	CD1	ILE	303	-11.163	-13.150	-4.960	1.00	17.60	ATOM	2452	CA	GLU	311	-6.596	-10.263	4.971	1.00	17.60
ATOM	2388	C	ILE	303	-8.100	-10.771	-2.706	1.00	17.60	ATOM	2453	CB	GLU	311	-5.242	-10.629	4.315	1.00	17.60
ATOM	2389	O	ILE	303	-8.383	-9.585	-2.696	1.00	17.60	ATOM	2454	CG	GLU	311	-5.257	-12.036	3.644	1.00	17.60
ATOM	2390	N	ALA	304	-8.336	-11.538	-1.620	1.00	17.60	ATOM	2455	CD	GLU	311	-4.553	-13.285	4.251	1.00	17.60
ATOM	2391	CA	ALA	304	-8.520	-11.002	-0.338	1.00	17.60	ATOM	2456	OE1	GLU	311	-4.936	-14.386	3.822	1.00	17.60
ATOM	2392	CB	ALA	304	-8.314	-12.051	0.716	1.00	17.60	ATOM	2457	OE2	GLU	311	-3.631	-13.210	5.086	1.00	17.60
ATOM	2393	C	ALA	304	-7.600	-9.809	-0.066	1.00	17.60	ATOM	2458	C	GLU	311	-6.424	-9.180	5.979	1.00	17.60
ATOM	2394	O	ALA	304	-8.028	-8.655	0.063	1.00	17.60	ATOM	2459	O	GLU	311	-5.955	-8.053	5.763	1.00	17.60
ATOM	2395	N	ILE	305	-6.298	-10.145	-0.231	1.00	17.60	ATOM	2460	N	ALA	312	-7.056	-9.429	7.091	1.00	17.60
ATOM	2396	CA	ILE	305	-5.263	-9.150	-0.049	1.00	17.60	ATOM	2461	CA	ALA	312	-6.953	-8.486	8.165	1.00	17.60
ATOM	2397	CB	ILE	305	-3.915	-9.813	-0.749	1.00	17.60	ATOM	2462	CB	ALA	312	-7.929	-8.076	9.278	1.00	17.60
ATOM	2398	CG2	ILE	305	-2.818	-8.960	-0.712	1.00	17.60	ATOM	2463	C	ALA	312	-5.693	-8.486	8.655	1.00	17.60
ATOM	2399	CG1	ILE	305	-3.624	-10.221	1.119	1.00	17.60	ATOM	2464	O	ALA	312	-4.815	-9.515	8.782	1.00	17.60
ATOM	2400	CD1	ILE	305	-2.614	-11.325	1.068	1.00	17.60	ATOM	2465	N	PRO	313	-5.008	-7.248	8.779	1.00	17.60
ATOM	2401	C	ILE	305	-3.462	-7.998	-0.988	1.00	17.60	ATOM	2466	CD	PRO	313	-5.764	-6.030	8.556	1.00	17.60
ATOM	2402	O	ILE	305	-5.806	-6.987	-0.489	1.00	17.60	ATOM	2467	CA	PRO	313	-3.676	-6.869	9.148	1.00	17.60

ATOM	2468	CB	PRO	313	-3.645	-5.424	9.398	1.00	17.60	ATOM	2533	CA	PRO	321	-5.899	7.269	15.661	1.00	17.60
ATOM	2469	CG	PRO	313	-5.116	-5.211	9.622	1.00	17.60	ATOM	2534	CB	PRO	321	-6.906	6.261	16.360	1.00	17.60
ATOM	2470	C	PRO	313	-3.234	-7.555	10.355	1.00	17.60	ATOM	2535	CG	PRO	321	-6.309	4.842	16.193	1.00	17.60
ATOM	2471	O	PRO	313	-3.640	-7.521	11.424	1.00	17.60	ATOM	2536	C	PRO	321	-5.218	8.309	16.385	1.00	17.60
ATOM	2472	N	PHE	314	-2.070	-8.111	10.111	1.00	17.60	ATOM	2537	O	PRO	321	-6.106	8.163	17.140	1.00	17.60
ATOM	2473	CA	PHE	314	-1.459	-8.058	11.143	1.00	17.60	ATOM	2538	N	GLY	322	-5.837	9.490	16.675	1.00	17.60
ATOM	2474	CB	PHE	314	-0.687	-9.945	10.418	1.00	17.60	ATOM	2539	CA	GLY	322	-5.702	10.583	17.415	1.00	17.60
ATOM	2475	CC	PHE	314	-1.746	-10.940	9.825	1.00	17.60	ATOM	2540	C	GLY	322	-5.061	11.607	16.191	1.00	17.60
ATOM	2476	CD	PHE	314	-1.567	-11.481	8.549	1.00	17.60	ATOM	2541	O	GLY	322	-6.055	11.970	15.689	1.00	17.60
ATOM	2477	CE	PHE	314	-2.963	-11.205	10.525	1.00	17.60	ATOM	2542	N	ASP	323	-3.882	11.210	15.652	1.00	17.60
ATOM	2478	CE	PHE	314	-2.585	-12.243	7.995	1.00	17.60	ATOM	2543	CA	ASP	323	-3.418	11.816	16.316	1.00	17.60
ATOM	2479	CE	PHE	314	-3.992	-11.977	9.962	1.00	17.60	ATOM	2544	CB	ASP	323	-4.033	13.295	16.140	1.00	17.60
ATOM	2480	CE	PHE	314	-3.790	-12.490	8.681	1.00	17.60	ATOM	2545	CG	ASP	323	-4.814	13.008	12.913	1.00	17.60
ATOM	2481	C	PHE	314	-0.726	-7.741	11.792	1.00	17.60	ATOM	2546	CO	ASP	323	-4.446	13.515	11.759	1.00	17.60
ATOM	2482	O	PHE	314	0.290	-7.267	11.315	1.00	17.60	ATOM	2547	CO	ASP	323	-5.753	14.592	13.159	1.00	17.60
ATOM	2483	N	ILE	315	-1.476	-7.265	12.775	1.00	17.60	ATOM	2548	C	ASP	323	-3.836	11.899	14.412	1.00	17.60
ATOM	2484	CA	ILE	315	-1.200	-6.168	13.644	1.00	17.60	ATOM	2549	O	ASP	323	-3.161	11.501	15.407	1.00	17.60
ATOM	2485	CB	ILE	315	-0.477	-6.673	14.910	1.00	17.60	ATOM	2550	N	THR	324	-3.436	12.349	13.205	1.00	17.60
ATOM	2486	CG	ILE	315	-0.766	-5.686	16.308	1.00	17.60	ATOM	2551	CA	THR	324	-0.230	13.086	12.903	1.00	17.60
ATOM	2487	CG	ILE	315	-1.027	-9.021	15.348	1.00	17.60	ATOM	2552	CB	THR	324	-0.750	16.616	12.979	1.00	17.60
ATOM	2488	CD	ILE	315	-0.018	-9.021	14.032	1.00	17.60	ATOM	2553	CO	THR	324	-1.975	16.756	12.200	1.00	17.60
ATOM	2489	C	ILE	315	-0.439	-5.104	12.934	1.00	17.60	ATOM	2554	CO	THR	324	0.221	15.626	12.350	1.00	17.60
ATOM	2490	O	ILE	315	-1.108	-4.628	12.030	1.00	17.60	ATOM	2555	C	THR	324	1.080	12.036	13.455	1.00	17.60
ATOM	2491	N	PRO	316	0.759	-4.541	13.195	1.00	17.60	ATOM	2556	O	THR	324	1.816	12.006	14.892	1.00	17.60
ATOM	2492	CD	PRO	316	1.780	-4.283	12.185	1.00	17.60	ATOM	2557	N	SER	325	2.202	12.046	12.892	1.00	17.60
ATOM	2493	CA	PRO	316	0.933	-3.524	14.218	1.00	17.60	ATOM	2558	CA	SER	325	3.552	12.566	13.424	1.00	17.60
ATOM	2494	CB	PRO	316	2.463	-3.333	14.272	1.00	17.60	ATOM	2559	CB	SER	325	4.023	12.859	14.231	1.00	17.60
ATOM	2495	CG	PRO	316	2.816	-3.332	12.812	1.00	17.60	ATOM	2560	CG	SER	325	4.010	15.035	13.469	1.00	17.60
ATOM	2496	C	PRO	316	0.161	-2.328	13.692	1.00	17.60	ATOM	2561	C	SER	325	3.532	11.445	14.328	1.00	17.60
ATOM	2497	O	PRO	316	-0.766	-1.306	13.318	1.00	17.60	ATOM	2562	O	SER	325	2.794	10.492	13.982	1.00	17.60
ATOM	2498	N	LYS	317	-1.395	-2.497	13.714	1.00	17.60	ATOM	2563	N	ASN	326	4.402	13.359	15.357	1.00	17.60
ATOM	2499	CA	LYS	317	-2.199	-2.611	13.141	1.00	17.60	ATOM	2564	CA	ASN	326	4.500	10.269	16.323	1.00	17.60
ATOM	2500	CB	LYS	317	-3.589	-2.209	13.411	1.00	17.60	ATOM	2565	CB	ASN	326	3.378	10.477	17.371	1.00	17.60
ATOM	2501	CG	LYS	317	-4.309	-2.788	12.194	1.00	17.60	ATOM	2566	CG	ASN	326	1.979	9.906	17.233	1.00	17.60
ATOM	2502	CD	LYS	317	-5.497	-3.739	12.510	1.00	17.60	ATOM	2567	CO	ASN	326	1.119	10.286	16.430	1.00	17.60
ATOM	2503	CE	LYS	317	-5.004	-5.115	13.118	1.00	17.60	ATOM	2568	CO	ASN	326	1.661	9.005	18.131	1.00	17.60
ATOM	2504	CE	LYS	317	-5.943	-6.251	13.130	1.00	17.60	ATOM	2569	C	ASN	326	6.569	7.889	16.631	1.00	17.60
ATOM	2505	C	LYS	317	-2.063	-0.255	13.757	1.00	17.60	ATOM	2570	O	ASN	326	6.556	8.026	15.024	1.00	17.60
ATOM	2506	O	LYS	317	-3.024	0.213	14.305	1.00	17.60	ATOM	2571	N	PHE	327	6.561	8.573	16.514	1.00	17.60
ATOM	2507	N	PHE	318	-0.938	0.394	13.563	1.00	17.60	ATOM	2572	CA	PHE	327	6.910	7.300	13.920	1.00	17.60
ATOM	2508	CA	PHE	318	-0.480	1.576	14.241	1.00	17.60	ATOM	2573	CB	PHE	327	3.775	6.794	13.133	1.00	17.60
ATOM	2509	CB	PHE	318	0.222	2.334	13.898	1.00	17.60	ATOM	2574	CG	PHE	327	2.819	6.144	16.059	1.00	17.60
ATOM	2510	CG	PHE	318	-0.833	3.184	12.472	1.00	17.60	ATOM	2575	CD	PHE	327	3.185	5.032	14.138	1.00	17.60
ATOM	2511	CD	PHE	318	-1.983	2.639	13.940	1.00	17.60	ATOM	2576	CD	PHE	327	1.565	6.637	14.184	1.00	17.60
ATOM	2512	CE	PHE	318	-0.798	4.514	12.652	1.00	17.60	ATOM	2577	CE	PHE	327	2.223	4.396	15.546	1.00	17.60
ATOM	2513	CE	PHE	318	-3.060	3.470	11.650	1.00	17.60	ATOM	2578	CE	PHE	327	0.677	5.989	15.002	1.00	17.60
ATOM	2514	CE	PHE	318	-1.874	5.372	12.349	1.00	17.60	ATOM	2579	C	PHE	327	1.014	4.873	15.678	1.00	17.60
ATOM	2515	C	PHE	318	-3.032	4.839	11.849	1.00	17.60	ATOM	2580	O	PHE	327	6.088	7.523	12.954	1.00	17.60
ATOM	2516	O	PHE	318	-1.529	2.398	15.079	1.00	17.60	ATOM	2581	N	ASP	328	6.736	6.606	12.415	1.00	17.60
ATOM	2517	N	GLY	319	-2.671	2.735	14.681	1.00	17.60	ATOM	2582	CA	ASP	328	6.236	8.803	12.697	1.00	17.60
ATOM	2518	CA	GLY	319	-1.110	2.836	16.269	1.00	17.60	ATOM	2583	CB	ASP	328	7.308	9.287	11.796	1.00	17.60
ATOM	2519	CB	GLY	319	-1.990	3.549	17.180	1.00	17.60	ATOM	2584	CG	ASP	328	6.631	10.208	10.723	1.00	17.60
ATOM	2520	CG	GLY	319	-1.265	3.695	18.504	1.00	17.60	ATOM	2585	CO	ASP	328	5.795	9.577	9.586	1.00	17.60
ATOM	2521	CO	GLY	319	-0.071	4.698	18.531	1.00	17.60	ATOM	2586	CO	ASP	328	6.358	9.082	8.611	1.00	17.60
ATOM	2522	C	GLY	319	1.096	4.260	19.454	1.00	17.60	ATOM	2587	CO	ASP	328	6.550	9.566	9.629	1.00	17.60
ATOM	2523	CE	GLY	319	1.457	2.791	19.216	1.00	17.60	ATOM	2588	C	ASP	328	8.183	9.955	12.915	1.00	17.60
ATOM	2524	CE	GLY	319	1.850	2.522	17.830	1.00	17.60	ATOM	2589	O	ASP	328	7.767	10.083	14.110	1.00	17.60
ATOM	2525	C	GLY	319	-2.514	4.892	16.750	1.00	17.60	ATOM	2590	N	ASP	329	9.418	10.356	12.526	1.00	17.60
ATOM	2526	O	GLY	319	-3.385	5.439	17.405	1.00	17.60	ATOM	2591	CA	ASP	329	10.464	10.915	13.401	1.00	17.60
ATOM	2527	N	GLY	320	-2.104	5.417	15.629	1.00	17.60	ATOM	2592	CB	ASP	329	11.750	10.306	12.999	1.00	17.60
ATOM	2528	CA	GLY	320	-2.475	6.773	15.254	1.00	17.60	ATOM	2593	CG	ASP	329	12.133	8.994	13.649	1.00	17.60
ATOM	2529	C	GLY	320	-3.778	6.923	14.473	1.00	17.60	ATOM	2594	CO	ASP	329	11.573	8.707	14.724	1.00	17.60
ATOM	2530	O	GLY	320	-3.816	7.575	13.412	1.00	17.60	ATOM	2595	CO	ASP	329	13.006	8.300	13.015	1.00	17.60
ATOM	2531	N	PRO	321	-4.883	6.396	15.031	1.00	17.60	ATOM	2596	C	ASP	329	10.663	12.423	13.528	1.00	17.60
ATOM	2532	CD	PRO	321	-5.317	4.979	16.919	1.00	17.60	ATOM	2597	O	ASP	329	9.893	13.259	13.019	1.00	17.60



ATOM	2598	N	TYR	330	11.741	12.786	14.227	1.00	17.60	ATOK	2663	C	ARG	336	31.953	27.996	1.567	1.00	17.60
ATOM	2599	CA	TYR	330	11.972	14.177	14.538	1.00	17.60	ATOM	2664	O	ARG	336	31.432	28.983	2.101	1.00	17.60
ATOM	2600	CB	TYR	330	12.007	14.434	16.123	1.00	17.60	ATOM	2665	N	VAL	337	32.629	28.114	0.594	1.00	17.60
ATOM	2601	CG	TYR	330	10.652	14.121	16.023	1.00	17.60	ATOM	2666	CA	VAL	337	33.143	29.386	0.013	1.00	17.60
ATOM	2602	CD	TYR	330	10.568	13.265	17.905	1.00	17.60	ATOM	2667	CB	VAL	337	14.587	29.705	0.264	1.00	17.60
ATOM	2603	CE	TYR	330	9.308	12.791	18.317	1.00	17.60	ATOM	2668	CG	VAL	337	14.587	30.548	1.573	1.00	17.60
ATOM	2604	CE2	TYR	330	9.477	14.521	16.208	1.00	17.60	ATOM	2669	CO	VAL	337	35.463	28.478	0.258	1.00	17.60
ATOM	2605	CE2	TYR	330	8.240	14.061	16.606	1.00	17.60	ATOM	2670	C	VAL	337	12.821	29.163	-1.442	1.00	17.60
ATOM	2606	CE	TYR	330	8.144	13.172	17.648	1.00	17.60	ATOM	2671	O	VAL	337	12.732	28.025	-1.899	1.00	17.60
ATOM	2607	OH	TYR	330	6.893	12.546	17.871	1.00	17.60	ATOM	2672	N	SEP	338	12.645	30.308	-2.099	1.00	17.60
ATOM	2608	C	TYR	330	13.292	14.453	13.815	1.00	17.60	ATOM	2673	CA	SEP	338	12.057	30.563	-3.426	1.00	17.60
ATOM	2609	O	TYR	330	14.370	13.877	14.058	1.00	17.60	ATOM	2674	CB	SEP	338	10.530	30.853	-3.269	1.00	17.60
ATOM	2610	N	GLU	331	13.100	15.282	12.808	1.00	17.60	ATOM	2675	OC	SEP	338	9.093	30.555	-1.935	1.00	17.60
ATOM	2611	CA	GLU	331	14.197	15.610	11.929	1.00	17.60	ATOM	2676	PD	SEP	338	9.414	31.632	-0.552	1.00	17.60
ATOM	2612	CB	GLU	331	13.690	15.335	10.505	1.00	17.60	ATOM	2677	OE1	SEP	338	9.167	31.005	-1.319	1.00	17.60
ATOM	2613	CG	GLU	331	12.859	14.063	10.306	1.00	17.60	ATOM	2678	OE2	SEP	338	8.203	30.915	0.230	1.00	17.60
ATOM	2614	CD	GLU	331	13.618	12.743	10.158	1.00	17.60	ATOM	2679	OE3	SEP	338	10.699	31.796	0.585	1.00	17.60
ATOM	2615	OE1	GLU	331	13.079	11.718	9.759	1.00	17.60	ATOM	2680	C	SEP	338	12.826	31.854	-2.754	1.00	17.60
ATOM	2616	OE2	GLU	331	14.796	12.714	10.433	1.00	17.60	ATOM	2681	O	SEP	338	12.917	32.652	-2.786	1.00	17.60
ATOM	2617	C	GLU	331	14.529	17.126	12.287	1.00	17.60	ATOM	2682	N	ILE	339	13.373	32.152	-4.970	1.00	17.60
ATOM	2618	O	GLU	331	13.720	17.866	12.806	1.00	17.60	ATOM	2683	CA	ILE	339	14.202	33.355	-5.306	1.00	17.60
ATOM	2619	IL	GLU	332	15.685	17.699	11.873	1.00	17.60	ATOM	2684	CB	ILE	339	15.741	32.948	-5.161	1.00	17.60
ATOM	2620	CA	GLU	332	15.093	19.140	12.046	1.00	17.60	ATOM	2685	CG	ILE	339	15.937	31.737	-6.038	1.00	17.60
ATOM	2621	CB	GLU	332	17.306	19.601	11.616	1.00	17.60	ATOM	2686	CG	ILE	339	16.759	34.049	-5.353	1.00	17.60
ATOM	2622	CD	GLU	332	17.689	19.481	10.313	1.00	17.60	ATOM	2687	CD	ILE	339	18.279	33.710	-5.501	1.00	17.60
ATOM	2623	CD	GLU	332	19.156	19.082	9.740	1.00	17.60	ATOM	2688	C	ILE	339	13.801	33.716	-6.744	1.00	17.60
ATOM	2624	OE1	GLU	332	19.314	18.418	8.620	1.00	17.60	ATOM	2689	O	ILE	339	12.614	31.493	-6.999	1.00	17.60
ATOM	2625	OE2	GLU	332	20.322	19.243	10.534	1.00	17.60	ATOM	2690	N	ASN	340	14.580	34.282	-7.718	1.00	17.60
ATOM	2626	C	GLU	332	14.883	19.832	11.137	1.00	17.60	ATOM	2691	CA	ASN	340	14.372	34.311	-9.159	1.00	17.60
ATOM	2627	O	GLU	332	14.435	19.231	10.139	1.00	17.60	ATOM	2692	CB	ASN	340	14.827	35.559	-9.881	1.00	17.60
ATOM	2628	IL	GLU	333	14.485	21.058	11.460	1.00	17.60	ATOM	2693	CG	ASN	340	14.420	35.937	-11.356	1.00	17.60
ATOM	2629	CA	GLU	333	13.579	21.717	10.572	1.00	17.60	ATOM	2694	OD	ASN	340	14.068	35.075	-12.170	1.00	17.60
ATOM	2630	CB	GLU	333	12.430	22.290	11.356	1.00	17.60	ATOM	2695	ND	ASN	340	14.489	37.182	-11.902	1.00	17.60
ATOM	2631	CG	GLU	333	11.310	21.527	10.672	1.00	17.60	ATOM	2696	C	ASN	340	14.619	32.955	-9.796	1.00	17.60
ATOM	2632	CD	GLU	333	10.355	21.049	11.533	1.00	17.60	ATOM	2697	O	ASN	340	14.791	31.981	-9.063	1.00	17.60
ATOM	2633	OE1	GLU	333	10.317	19.866	11.940	1.00	17.60	ATOM	2698	N	GLU	341	14.887	33.702	-11.069	1.00	17.60
ATOM	2634	OE2	GLU	333	9.287	21.899	11.751	1.00	17.60	ATOM	2699	CA	GLU	341	15.882	31.351	-11.568	1.00	17.60
ATOM	2635	C	GLU	333	14.437	22.761	9.924	1.00	17.60	ATOM	2700	CB	GLU	341	14.383	31.317	-12.888	1.00	17.60
ATOM	2636	O	GLU	333	15.286	23.426	10.554	1.00	17.60	ATOM	2701	CG	GLU	341	13.819	29.935	-12.990	1.00	17.60
ATOM	2637	N	GLU	334	14.197	22.855	8.624	1.00	17.60	ATOM	2702	CD	GLU	341	12.619	29.889	-13.913	1.00	17.60
ATOM	2638	CA	GLU	334	15.012	23.686	7.747	1.00	17.60	ATOM	2703	OE1	GLU	341	11.542	29.693	-13.319	1.00	17.60
ATOM	2639	CB	GLU	334	15.896	22.635	6.922	1.00	17.60	ATOM	2704	OE2	GLU	341	12.743	30.049	-15.146	1.00	17.60
ATOM	2640	CG	GLU	334	15.374	21.289	6.242	1.00	17.60	ATOM	2705	C	GLU	341	16.403	30.601	-11.691	1.00	17.60
ATOM	2641	CD	GLU	334	15.037	20.031	7.088	1.00	17.60	ATOM	2706	O	GLU	341	17.354	30.982	-12.352	1.00	17.60
ATOM	2642	OE1	GLU	334	15.818	19.038	7.193	1.00	17.60	ATOM	2707	N	LYS	342	16.254	29.634	-11.068	1.00	17.60
ATOM	2643	OE2	GLU	334	13.919	19.952	7.633	1.00	17.60	ATOM	2708	CA	LYS	342	17.327	28.514	-10.914	1.00	17.60
ATOM	2644	C	GLU	334	14.080	24.619	6.932	1.00	17.60	ATOM	2709	CB	LYS	342	17.230	27.811	-9.614	1.00	17.60
ATOM	2645	O	GLU	334	12.859	24.453	7.354	1.00	17.60	ATOM	2710	CG	LYS	342	18.263	28.512	-8.749	1.00	17.60
ATOM	2646	N	ILE	335	14.403	25.596	6.042	1.00	17.60	ATOM	2711	CD	LYS	342	17.913	30.070	-8.436	1.00	17.60
ATOM	2647	CA	ILE	335	13.286	26.267	5.393	1.00	17.60	ATOM	2712	CE	LYS	342	19.109	30.900	-7.996	1.00	17.60
ATOM	2648	CB	ILE	335	13.236	27.628	6.034	1.00	17.60	ATOM	2713	NE	LYS	342	20.128	31.192	-9.034	1.00	17.60
ATOM	2649	CD	ILE	335	14.160	28.638	5.269	1.00	17.60	ATOM	2714	C	LYS	342	17.186	27.197	-12.035	1.00	17.60
ATOM	2650	CO	ILE	335	11.743	27.994	6.863	1.00	17.60	ATOM	2715	O	LYS	342	18.409	27.705	-12.705	1.00	17.60
ATOM	2651	CD	ILE	335	11.276	29.183	7.003	1.00	17.60	ATOM	2716	N	CSH	343	16.768	26.397	-12.227	1.00	17.60
ATOM	2652	C	ILE	335	13.350	26.344	3.867	1.00	17.60	ATOM	2717	CA	CSH	343	17.137	25.671	-13.427	1.00	17.60
ATOM	2653	O	ILE	335	16.132	26.260	3.116	1.00	17.60	ATOM	2718	CB	CSH	343	17.798	24.331	-13.102	1.00	17.60
ATOM	2654	N	ARG	336	18.908	26.462	3.372	1.00	17.60	ATOM	2719	SO	CSH	343	18.799	24.279	-11.615	1.00	17.60
ATOM	2655	CA	ARG	336	11.618	26.564	1.950	1.00	17.60	ATOM	2720	C	CSH	343	15.920	25.450	-14.297	1.00	17.60
ATOM	2656	CB	ARG	336	10.204	26.331	1.558	1.00	17.60	ATOM	2721	O	CSH	343	15.382	24.331	-14.396	1.00	17.60
ATOM	2657	CG	ARG	336	9.517	25.012	1.896	1.00	17.60	ATOM	2722	N	GLY	344	15.567	26.484	-15.078	1.00	17.60
ATOM	2658	CD	ARG	336	8.013	25.304	1.463	1.00	17.60	ATOM	2723	CA	GLY	344	14.384	26.421	-15.932	1.00	17.60
ATOM	2659	NE	ARG	336	6.930	25.461	2.418	1.00	17.60	ATOM	2724	C	GLY	344	14.376	25.332	-17.001	1.00	17.60
ATOM	2660	C2	ARG	336	6.183	26.701	2.548	1.00	17.60	ATOM	2725	O	GLY	344	13.503	26.458	-16.590	1.00	17.60
ATOM	2661	HN	ARG	336	6.771	27.796	1.837	1.00	17.60	ATOM	2726	N	LYS	345	15.384	25.342	-17.895	1.00	17.60
ATOM	2662	HN2	ARG	336	5.294	26.020	3.298	1.00	17.60	ATOM	2727	CA	LYS	345	15.378	24.432	-19.053	1.00	17.60

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ATOM	2720	CA	LYS	345	16.550	24.757	-20.001	1.00	17.60	23.791	-12.917	13.103	1.00	17.60
ATOM	2729	CG	LYS	345	16.639	26.169	-20.707	1.00	17.60	24.247	-16.257	13.192	1.00	17.60
ATOM	2730	CD	LYS	345	15.143	26.300	-21.605	1.00	17.60	24.243	-12.365	13.192	1.00	17.60
ATOM	2731	CE	LYS	345	14.701	27.680	-22.296	1.00	17.60	23.664	-10.863	14.572	1.00	17.60
ATOM	2732	CE	LYS	345	15.570	28.070	-23.478	1.00	17.60	24.125	-9.768	14.206	1.00	17.60
ATOM	2733	C	LYS	345	15.444	22.975	-18.680	1.00	17.60	22.575	-10.972	15.330	1.00	17.60
ATOM	2734	O	LYS	345	14.965	22.116	-19.386	1.00	17.60	21.774	-9.030	15.710	1.00	17.60
ATOM	2735	N	GLU	346	15.951	22.728	-17.494	1.00	17.60	20.659	-10.292	16.639	1.00	17.60
ATOM	2736	CA	GLU	346	16.142	21.306	-16.960	1.00	17.60	19.081	-9.352	16.580	1.00	17.60
ATOM	2737	CB	GLU	346	17.187	21.506	-15.880	1.00	17.60	19.088	-8.100	17.295	1.00	17.60
ATOM	2738	CG	GLU	346	18.431	22.078	-16.553	1.00	17.60	18.415	-7.293	17.099	1.00	17.60
ATOM	2739	CD	GLU	346	18.900	23.495	-16.229	1.00	17.60	18.410	-9.650	15.711	1.00	17.60
ATOM	2740	CE	GLU	346	20.007	23.585	-15.707	1.00	17.60	17.381	-8.779	15.515	1.00	17.60
ATOM	2741	CE	GLU	346	14.066	20.690	-16.446	1.00	17.60	17.400	-7.509	16.211	1.00	17.60
ATOM	2742	C	GLU	346	14.562	19.536	-16.000	1.00	17.60	16.387	-6.644	15.997	1.00	17.60
ATOM	2743	O	GLU	346	14.120	21.484	-15.632	1.00	17.60	22.722	-8.907	16.436	1.00	17.60
ATOM	2744	N	PHE	347	12.931	21.043	-15.949	1.00	17.60	22.079	-7.780	15.960	1.00	17.60
ATOM	2745	CA	PHE	347	13.049	21.421	-13.529	1.00	17.60	23.427	-9.306	17.478	1.00	17.60
ATOM	2746	CB	PHE	347	16.260	20.770	-12.950	1.00	17.60	24.381	-8.602	18.240	1.00	17.60
ATOM	2747	CG	PHE	347	15.403	21.513	-12.844	1.00	17.60	25.160	-9.389	19.238	1.00	17.60
ATOM	2748	CD	PHE	347	14.208	19.466	-12.588	1.00	17.60	25.016	-8.040	17.325	1.00	17.60
ATOM	2749	CE	PHE	347	16.546	20.913	-12.371	1.00	17.60	25.914	-6.980	17.654	1.00	17.60
ATOM	2750	CE	PHE	347	15.355	18.893	-12.310	1.00	17.60	25.706	-8.667	16.195	1.00	17.60
ATOM	2751	CE	PHE	347	16.521	19.606	-12.012	1.00	17.60	26.756	-8.021	15.301	1.00	17.60
ATOM	2752	C	PHE	347	11.677	21.654	-15.524	1.00	17.60	27.351	-8.029	14.329	1.00	17.60
ATOM	2753	O	PHE	347	10.773	22.080	-14.011	1.00	17.60	28.176	-10.069	15.078	1.00	17.60
ATOM	2754	N	THR	348	11.633	21.689	-16.049	1.00	17.60	29.318	-9.815	15.673	1.00	17.60
ATOM	2755	CA	THR	348	10.522	22.291	-17.545	1.00	17.60	26.156	-6.065	14.515	1.00	17.60
ATOM	2756	CB	THR	348	10.970	22.743	-18.977	1.00	17.60	26.765	-5.790	14.356	1.00	17.60
ATOM	2757	CG	THR	348	11.925	21.089	-19.494	1.00	17.60	24.920	-7.038	14.072	1.00	17.60
ATOM	2758	CD	THR	348	11.285	24.205	-18.945	1.00	17.60	24.275	-5.971	13.364	1.00	17.60
ATOM	2759	C	THR	348	9.269	21.458	-17.680	1.00	17.60	22.947	-6.491	12.044	1.00	17.60
ATOM	2760	O	THR	348	8.185	22.040	-17.743	1.00	17.60	22.159	-5.551	11.960	1.00	17.60
ATOM	2761	N	GLU	349	9.349	20.342	-17.730	1.00	17.60	22.710	-5.033	10.815	1.00	17.60
ATOM	2762	CA	GLU	349	8.388	19.301	-17.962	1.00	17.60	20.879	-5.246	12.306	1.00	17.60
ATOM	2763	CB	GLU	349	7.851	17.036	-19.108	1.00	17.60	20.014	-4.200	9.981	1.00	17.60
ATOM	2764	CG	GLU	349	8.581	15.690	-19.016	1.00	17.60	20.700	-3.090	10.318	1.00	17.60
ATOM	2765	CD	GLU	349	9.316	15.355	-19.964	1.00	17.60	24.079	-4.758	16.274	1.00	17.60
ATOM	2766	CE	GLU	349	8.412	16.981	-19.997	1.00	17.60	24.411	-3.666	13.822	1.00	17.60
ATOM	2767	CE	GLU	349	7.629	18.855	-19.604	1.00	17.60	23.645	-4.065	15.533	1.00	17.60
ATOM	2768	C	GLU	349	7.462	17.668	-16.330	1.00	17.60	23.277	-3.695	16.366	1.00	17.60
ATOM	2769	O	GLU	349	7.354	19.766	-15.704	1.00	17.60	22.452	-4.092	17.593	1.00	17.60
ATOM	2770	N	PHE	350	6.982	19.393	-14.376	1.00	17.60	21.124	-4.485	17.047	1.00	17.60
ATOM	2771	CA	PHE	350	8.291	19.497	-13.503	1.00	17.60	22.954	-5.265	18.382	1.00	17.60
ATOM	2772	CB	PHE	350	8.275	18.888	-12.078	1.00	17.60	24.120	-5.306	19.429	1.00	17.60
ATOM	2773	CG	PHE	350	7.306	19.222	-11.164	1.00	17.60	24.362	-2.800	16.052	1.00	17.60
ATOM	2774	CD	PHE	350	9.206	17.930	-11.758	1.00	17.60	24.145	-1.714	17.374	1.00	17.60
ATOM	2775	C	PHE	350	7.253	18.605	-9.914	1.00	17.60	25.527	-3.387	16.658	1.00	17.60
ATOM	2776	CE	PHE	350	9.149	17.315	-10.527	1.00	17.60	26.812	-2.773	16.074	1.00	17.60
ATOM	2777	CE	PHE	350	8.179	17.614	-9.609	1.00	17.60	27.706	-3.080	17.370	1.00	17.60
ATOM	2778	C	PHE	350	5.877	20.337	-13.926	1.00	17.60	27.370	-2.116	15.569	1.00	17.60
ATOM	2779	O	PHE	350	5.936	21.507	-14.301	1.00	17.60	28.382	-1.398	15.623	1.00	17.60
ATOM	2780	N	THR	351	5.019	19.939	-13.318	1.00	17.60	26.787	-2.249	16.366	1.00	17.60
ATOM	2781	CA	THR	351	26.441	-13.459	17.857	1.00	17.60	27.347	-1.619	13.177	1.00	17.60
ATOM	2782	CB	THR	351	25.021	-13.729	17.829	1.00	17.60	27.190	-2.614	12.067	1.00	17.60
ATOM	2783	CG	THR	351	24.686	-13.256	19.195	1.00	17.60	25.853	-2.979	11.925	1.00	17.60
ATOM	2784	CD	THR	351	23.469	-12.380	18.814	1.00	17.60	26.536	-0.881	12.895	1.00	17.60
ATOM	2785	C	THR	351	25.504	-12.532	20.177	1.00	17.60	25.464	-0.262	13.462	1.00	17.60
ATOM	2786	O	THR	351	24.785	-12.806	16.655	1.00	17.60	27.052	0.284	11.918	1.00	17.60
ATOM	2787	N	GLY	352	25.320	-11.641	16.067	1.00	17.60	26.463	1.519	11.458	1.00	17.60
ATOM	2788	CA	GLY	352	24.295	-13.136	15.672	1.00	17.60	25.270	1.100	10.553	1.00	17.60
ATOM	2789	CB	GLY	352	24.364	-12.206	14.339	1.00	17.60	24.670	2.271	10.439	1.00	17.60
ATOM	2790	CG	GLY	352						24.983	0.151			



ATOM	2857	CA	ARG	361	23.026	0.011	9.034	1.00	17.60	ATOM	2922	CA	MIS	369	24.319	6.602	-5.795	1.00	17.60
ATOM	2858	CB	ARG	361	23.953	-1.239	0.119	1.00	17.60	ATOM	2923	CB	MIS	369	23.365	6.052	-7.740	1.00	17.60
ATOM	2859	CG	ARG	361	25.149	-1.350	7.129	1.00	17.60	ATOM	2924	CG	MIS	369	23.162	6.072	-9.024	1.00	17.60
ATOM	2860	CD	ARG	361	25.502	-0.300	6.169	1.00	17.60	ATOM	2925	CD	MIS	369	21.953	7.571	-9.335	1.00	17.60
ATOM	2861	CE	ARG	361	24.559	0.237	5.204	1.00	17.60	ATOM	2926	CE	MIS	369	26.063	7.167	-9.937	1.00	17.60
ATOM	2862	CF	ARG	361	24.592	1.425	4.612	1.00	17.60	ATOM	2927	CE	MIS	369	23.459	7.907	-10.703	1.00	17.60
ATOM	2863	CH	ARG	361	25.602	2.259	4.899	1.00	17.60	ATOM	2928	CE	MIS	369	22.193	8.212	-10.634	1.00	17.60
ATOM	2864	CI	ARG	361	23.509	1.799	3.796	1.00	17.60	ATOM	2929	C	MIS	369	26.022	8.162	-6.829	1.00	17.60
ATOM	2865	C	ARG	361	22.467	-0.095	9.718	1.00	17.60	ATOM	2930	O	MIS	369	22.930	8.697	-6.651	1.00	17.60
ATOM	2866	O	ARG	361	21.510	-0.504	9.092	1.00	17.60	ATOM	2931	N	ASP	370	23.077	8.621	-7.475	1.00	17.60
ATOM	2867	K	THR	362	22.365	0.202	11.002	1.00	17.60	ATOM	2932	CA	ASP	370	25.319	9.962	-8.033	1.00	17.60
ATOM	2868	CA	THR	362	21.116	0.199	11.746	1.00	17.60	ATOM	2933	CB	ASP	370	25.602	11.006	-6.046	1.00	17.60
ATOM	2869	CB	THR	362	23.414	0.053	13.275	1.00	17.60	ATOM	2934	CG	ASP	370	25.040	10.621	-5.425	1.00	17.60
ATOM	2870	CG	THR	362	22.340	1.035	13.731	1.00	17.60	ATOM	2935	CG	ASP	370	23.031	10.619	-5.222	1.00	17.60
ATOM	2871	CG	THR	362	21.917	-1.349	13.524	1.00	17.60	ATOM	2936	CG	ASP	370	25.779	10.219	-4.512	1.00	17.60
ATOM	2872	C	THR	362	20.275	1.427	13.468	1.00	17.60	ATOM	2937	C	ASP	370	26.590	9.434	-8.045	1.00	17.60
ATOM	2873	O	THR	362	19.060	1.460	13.657	1.00	17.60	ATOM	2938	O	ASP	370	27.703	9.719	-8.502	1.00	17.60
ATOM	2874	N	GLY	363	21.009	2.457	13.006	1.00	17.60	ATOM	2939	OXT	ASP	370	26.366	8.539	-9.720	1.00	17.60
ATOM	2875	CA	GLY	363	20.440	3.747	10.657	1.00	17.60	TER									
ATOM	2876	C	GLY	363	19.450	3.604	9.510	1.00	17.60										
ATOM	2877	O	GLY	363	19.103	2.508	9.020	1.00	17.60										
ATOM	2878	N	ARG	364	18.004	4.685	9.073	1.00	17.60										
ATOM	2879	CA	ARG	364	17.907	6.653	7.892	1.00	17.60										
ATOM	2880	CB	ARG	364	17.061	5.030	7.067	1.00	17.60										
ATOM	2881	CD	ARG	364	15.050	5.375	8.638	1.00	17.60										
ATOM	2882	CE	ARG	364	14.635	6.221	8.675	1.00	17.60										
ATOM	2883	CE	ARG	364	16.157	6.592	7.337	1.00	17.60										
ATOM	2884	CE	ARG	364	14.099	7.070	6.919	1.00	17.60										
ATOM	2885	CH	ARG	364	14.464	8.060	7.811	1.00	17.60										
ATOM	2886	CH	ARG	364	13.793	8.107	5.604	1.00	17.60										
ATOM	2887	C	ARG	364	19.075	4.752	6.955	1.00	17.60										
ATOM	2888	O	ARG	364	19.910	5.658	6.056	1.00	17.60										
ATOM	2889	N	ARG	365	19.152	3.717	6.052	1.00	17.60										
ATOM	2890	CA	ARG	365	20.194	3.506	5.075	1.00	17.60										
ATOM	2891	CB	ARG	365	20.235	3.320	6.767	1.00	17.60										
ATOM	2892	CD	ARG	365	20.533	1.432	5.999	1.00	17.60										
ATOM	2893	CE	ARG	365	20.355	-0.009	5.766	1.00	17.60										
ATOM	2894	CE	ARG	365	19.066	-0.376	5.249	1.00	17.60										
ATOM	2895	CE	ARG	365	18.127	-0.945	5.981	1.00	17.60										
ATOM	2896	CH	ARG	365	16.874	-1.203	3.440	1.00	17.60										
ATOM	2897	CH	ARG	365	18.275	-1.111	7.290	1.00	17.60										
ATOM	2898	C	ARG	365	19.809	4.509	3.007	1.00	17.60										
ATOM	2899	O	ARG	365	18.780	4.551	3.299	1.00	17.60										
ATOM	2900	N	ASN	366	20.047	5.361	3.509	1.00	17.60										
ATOM	2901	CA	ASN	366	20.621	6.231	2.453	1.00	17.60										
ATOM	2902	CB	ASN	366	21.567	7.204	2.628	1.00	17.60										
ATOM	2903	CD	ASN	366	20.706	0.492	2.470	1.00	17.60										
ATOM	2904	CE	ASN	366	20.544	9.037	1.342	1.00	17.60										
ATOM	2905	CE	ASN	366	20.007	8.840	3.616	1.00	17.60										
ATOM	2906	C	ASN	366	20.762	5.546	1.139	1.00	17.60										
ATOM	2907	O	ASN	366	21.353	4.461	1.009	1.00	17.60										
ATOM	2908	N	ALA	367	20.271	6.203	0.000	1.00	17.60										
ATOM	2909	CA	ALA	367	20.282	3.676	-1.294	1.00	17.60										
ATOM	2910	CB	ALA	367	19.127	6.172	-2.170	1.00	17.60										
ATOM	2911	C	ALA	367	21.517	6.095	-2.034	1.00	17.60										
ATOM	2912	O	ALA	367	21.059	7.269	-3.950	1.00	17.60										
ATOM	2913	N	ILE	368	22.151	5.154	-2.719	1.00	17.60										
ATOM	2914	CA	ILE	368	23.369	5.460	-3.450	1.00	17.60										
ATOM	2915	CB	ILE	368	24.241	4.230	-3.703	1.00	17.60										
ATOM	2916	CG	ILE	368	25.052	6.315	-2.455	1.00	17.60										
ATOM	2917	CG	ILE	368	23.629	2.930	-4.076	1.00	17.60										
ATOM	2918	CD	ILE	368	24.677	2.102	-4.870	1.00	17.60										
ATOM	2919	C	ILE	368	23.301	6.060	-4.806	1.00	17.60										
ATOM	2920	O	ILE	368	22.151	6.507	-5.226	1.00	17.60										
ATOM	2921	N	MIS	369	24.324	6.102	-5.593	1.00	17.60										

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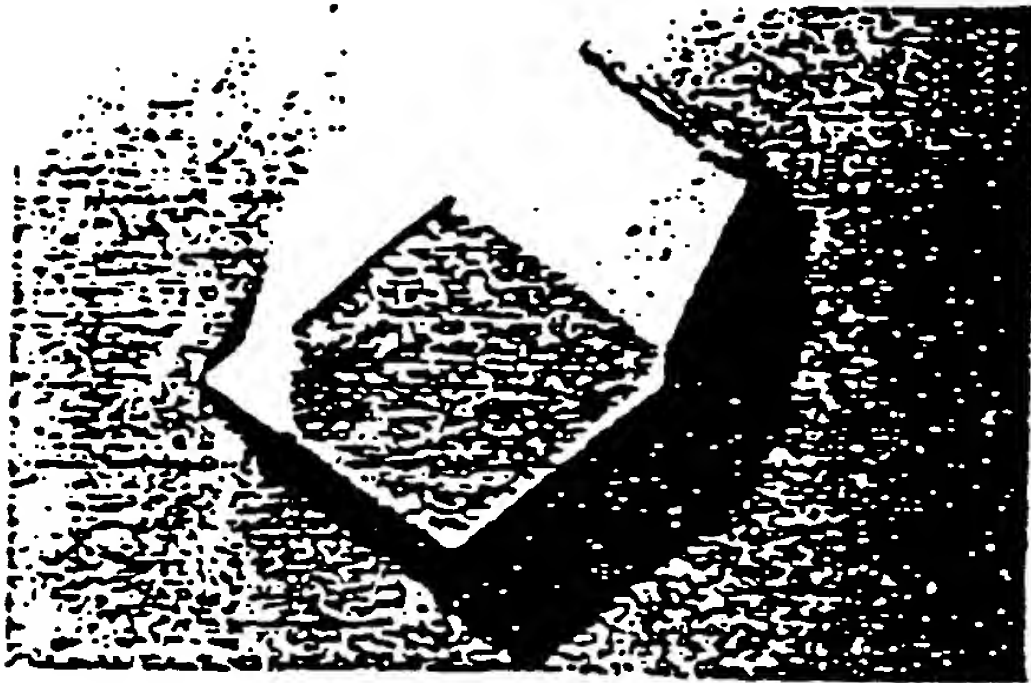


FIGURE 18A

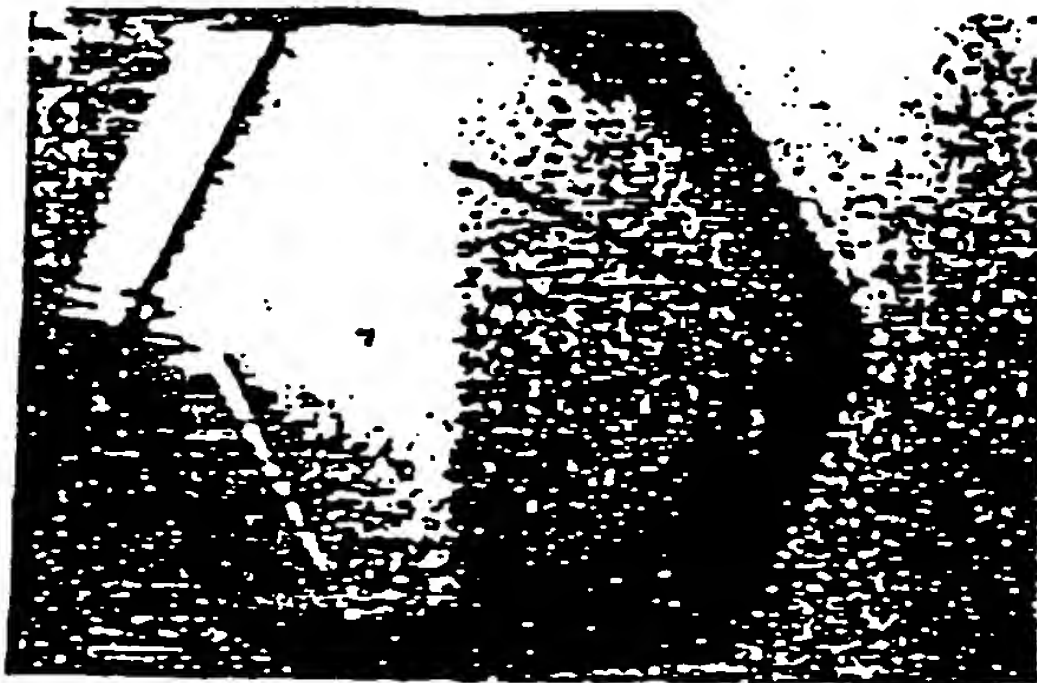


FIGURE 18B

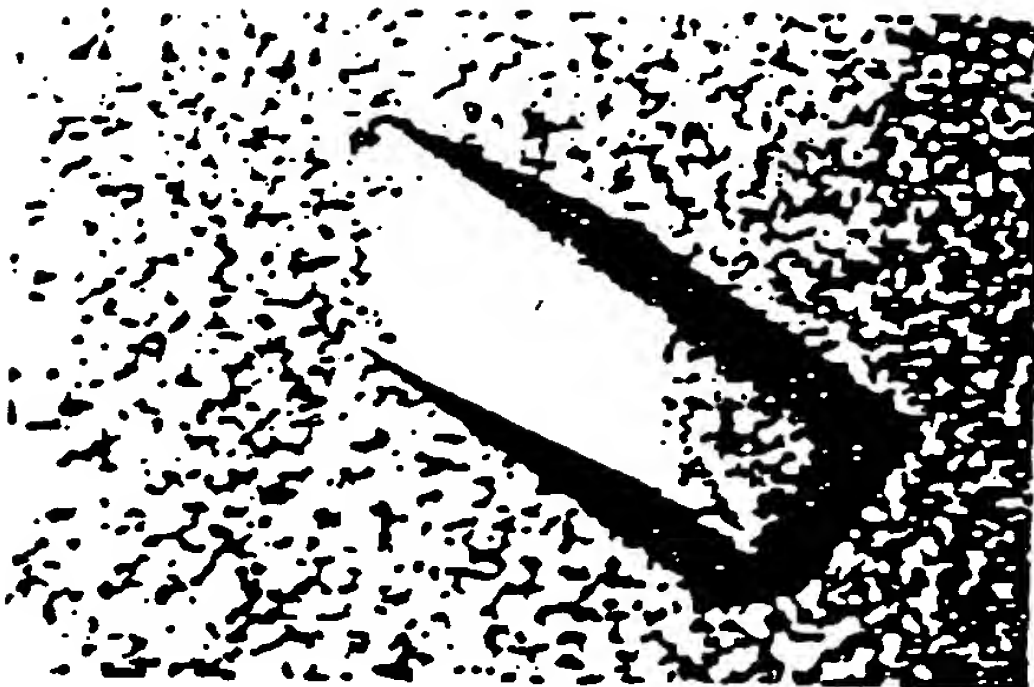


FIGURE 18C

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TABLE 1 Structure Solution Statistics

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(a). Diffraction Data:

Data Sets	No. of Crystals	d <sub>min</sub> (Å)	No. of Measurements	No. of Reflections	<I/σ(I)>	Completeness (%)	R <sub>sym</sub>
Native-1	2	2.7	58889	12713	12.9	98.1	0.061
Native-2	1	2.7	27067	11291	13.2	87.3	0.040
PIIMB-1	1	3.0	30973	7233	13.3	76.1	0.063
PIIMB-2	1	3.0	23476	8809	6.9	92.1	0.075
MgATP	1	2.7	26464	11840	11.1	91.1	0.048

(b) SIRAS Phasing Statistics:

	Overall	11.72	7.70	6.11	5.22	4.63	4.20	3.87	3.61
Mean figure of merit	0.57	0.74	0.75	0.68	0.62	0.55	0.53	0.47	0.43
PIIMB-1									
acentric r.m.s. f <sub>h</sub> /E <sub>iso</sub>	2.73	3.27	3.80	3.70	3.00	2.54	2.56	2.26	2.05
r.m.s. ΔF <sub>anom</sub> /E <sub>anom</sub>	0.96	1.53	1.68	1.41	1.19	1.05	0.89	0.78	0.60
R <sub>c</sub>	0.50	0.34	0.38	0.45	0.51	0.78	0.64	0.70	0.81
PIIMB-2									
acentric r.m.s. f <sub>h</sub> /E <sub>iso</sub>	2.26	3.89	3.72	3.35	2.81	2.34	2.08	1.83	1.51
R <sub>c</sub>	0.60	0.37	0.53	0.58	0.64	0.75	0.71	0.65	0.61

(c) Refinement:

Model	No. of Residues/Chains	Initial R-factor	Final R-factor	B	Data Selection
A. First unrefined partial	275/4	0.473	0.304	overall	10-2.7 Å, F/σ > 2
B. First unrefined full	356/2	0.434	0.228	overall	10-2.7 Å, F/σ > 2
C. Latest X-PLOR	356/2	—	0.195	individual	10-2.7 Å, F/σ > 2
D. TNT	356/2	0.221	0.212	individual	40-2.7 Å



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TABLE 3

<u>POINTS OF CONTACT</u>	<u>POSITION</u>	<u>CAPK</u>	<u>CKII</u>
P+1	197	Thr	Val
	198	Leu	Arg
	199	Cys	Val
	200	Gly	Ala
	201	Thr	Ser
	202	Pro	Arg
	203	Glu	Tyr
	204	Tyr	Phe
	205	Leu	Lys
P-2	170	Glu	His
	230	Glu	Glu
P-3	127	Glu	Asp
	331	Glu	
P-6	203	Leu	
P-11	235	Tyr	
	236	Pro	
	237	Pro	
	238	Phe	
	239	Phe	



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TABLE 4

Angstroms apart	Atom 1	Atom 2
5.29	ASP 184 CA	GLY 186 CA
5.73	GLU 91 CA	GLY 186 CA
6.46	ASN 171 CA	ASP 184 CA
7.41	ASN 171 CA	ASP 166 CA
7.61	ASP 166 CA	GLY 186 CA
7.87	ASP 184 CA	GLU 91 CA
8.20	ASP 166 CA	ASP 184 CA
9.20	ASP 184 CA	LYS 72 CA
9.90	GLY 52 CA	LYS 72 CA
10.15	ASN 171 CA	GLY 186 CA
10.29	ASP 184 CA	GLY 52 CA
10.53	GLY 52 CA	GLY 186 CA
10.78	ASN 171 CA	GLY 52 CA
10.91	GLY 186 CA	LYS 72 CA
11.29	GLU 91 CA	LYS 72 CA
11.80	ARG 280 CA	GLU 208 CA
12.27	ASP 166 CA	GLU 91 CA
12.65	ASP 166 CA	GLY 52 CA
13.52	ASN 171 CA	LYS 72 CA
14.07	ASN 171 CA	GLU 91 CA
15.02	GLU 91 CA	GLY 52 CA
15.07	ASP 166 CA	GLU 208 CA
16.54	ASP 166 CA	LYS 72 CA
18.58	ARG 280 CA	ASP 166 CA
19.99	GLU 208 CA	GLY 186 CA
22.00	ASN 171 CA	GLU 208 CA
22.82	ASP 184 CA	GLU 208 CA
23.37	GLU 91 CA	GLU 208 CA
23.49	ARG 280 CA	ASN 171 CA
24.87	ARG 280 CA	GLY 186 CA
25.18	GLU 208 CA	GLY 52 CA
25.61	ARG 280 CA	ASP 184 CA
27.34	ARG 280 CA	GLU 91 CA
30.53	GLU 208 CA	LYS 72 CA
30.83	ARG 280 CA	GLY 52 CA
34.67	ARG 280 CA	LYS 72 CA

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 92/06137

**I. CLASSIFICATION OF SUBJECT MATTER** (if several classification symbols apply, indicate all)<sup>6</sup>

According to International Patent Classification (IPC) or to both National Classification and IPC

Int.Cl. 5 C12Q1/00; C12Q1/48; C12N9/99; G01N33/68  
C07K13/00; A61K37/64; C07K15/00

**II. FIELDS SEARCHED**Minimum Documentation Searched<sup>7</sup>

Classification System

Classification Symbols

Int.Cl. 5 C12Q ; C12N ; G01N ; A61K  
C07K

Documentation Searched other than Minimum Documentation  
to the Extent that such Documents are Included in the Fields Searched<sup>8</sup>**III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup>**

Category <sup>10</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
------------------------	--	-------------------------------------

A	WO,A,8 907 654 (PROGENICS PHARMACEUTICALS) 24 August 1989 see claims; example 1	1
A	EP,A,0 359 981 (BOEHRINGER) 28 March 1990 see claims	1,29

<sup>10</sup> Special categories of cited documents:

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- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "A" document member of the same patent family

**IV. CERTIFICATION**

Date of the Actual Completion of the International Search

04 NOVEMBER 1992

Date of Mailing of this International Search Report

16. 11. 92

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer

DELANGHE L.L.M.

## III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
A	<p>CHEMICAL ABSTRACTS, vol. 105, no. 21, 24 November 1986, Columbus, Ohio, US; abstract no. 186487d, CLORE, G.MARIUS ET AL. 'Stereochemistry of binding of the tetrapeptide acetyl-Pro-Ala-Pro-Tyr-NH<sub>2</sub> to porcine pancreatic elastase. Combined use of two-dimensional transferred nuclear Overhauser enhancement measurements, restrained molecular dynamics, X-ray crystallography and molecular modelling.' page 314 ; see abstract &amp; J.MOL.BIOL. vol. 190, no. 2, 1986, ENG pages 259 - 267</p>	1
P, X	<p>--- CHEMICAL ABSTRACTS, vol. 115, no. 13, 30 September 1991, Columbus, Ohio, US; abstract no. 130637s, KNIGHTON, DANIEL R. ET AL. 'Crystallization of cAMP-dependent protein kinase. Cocystals of the catalytic subunit with a 20 amino acid residue peptide inhibitor and magnesium-ATP diffract to 3.0 Å resolution.' page 453 ; see abstract &amp; J.MOL.BIOL. vol. 220, no. 2, 1991, ENG pages 217 - 220</p>	1
P, X	<p>--- SCIENCE vol. 253, no. 5018, 26 July 1991, LANCASTER, PA US pages 414 - 420 D.R.KNIGHTON ET AL. 'Structure of a peptide inhibitor bound to the catalytic subunit of cyclic adenosine monophosphate-dependent protein kinase.' see page 420 see the whole document</p> <p>-----</p>	1-66

**ANNEX TO THE INTERNATIONAL SEARCH REPORT  
ON INTERNATIONAL PATENT APPLICATION NO. US 9206137  
SA 62983**

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.  
The members are as contained in the European Patent Office EDP file on  
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Patent document cited in search report	Publication date	Patent family member(s)	Publication date	
WO-A-8907654	24-08-89	US-A-	4980281	25-12-90
		AU-B-	612948	18-07-91
		AU-A-	3184089	06-09-89
		EP-A-	0403506	27-12-90
		JP-T-	3503598	15-08-91
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EP-A-0359981	28-03-90	DE-A-	3827974	22-02-90
		AU-B-	627207	20-08-92
		AU-A-	3955089	22-02-90
		JP-A-	2108636	20-04-90
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